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【発明の名称】　高温耐性コリネ型細菌の耐熱性アミノ酸生合成系酵素遺伝子

【請求項の数】　14

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出証特２０００－３０９３６１３

【書類名】　明細書

【発明の名称】　高温耐性コリネ型細菌の耐熱性アミノ酸生合成系酵素遺伝子

【特許請求の範囲】

【請求項１】　配列番号２に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソシトレートリアーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項２】　配列番号４に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アシルＣｏ－Ａカルボキシラーゼ活性に関与するタンパク質をコードするＤＮＡ。

【請求項３】　配列番号６に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ＤｔｓＲ活性を有するタンパク質をコードするＤＮＡ。

【請求項４】　配列番号８に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ＤｔｓＲ活性を有するタンパク質をコードするＤＮＡ。

【請求項５】　配列番号１０に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホフルクトキナーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項６】　配列番号１２又は１４に記載のアミノ酸配列、又は、前記アミノ酸配列のいずれかにおいて、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列を含み、かつ、インベルターゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項７】　配列番号１７～２０に記載のアミノ酸配列のいずれかを有するタンパク質、又は、前記アミノ酸配列のいずれかにおいて、１若しくは数個の

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アミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、グルタミン酸の取り込みに関与する機能を有するタンパク質、をコードするＤＮＡ。

【請求項８】　配列番号２２に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸デヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項９】　配列番号２４に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項１０】　配列番号２６に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホエノールピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項１１】　配列番号２８に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アコニターゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項１２】　配列番号３０に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソクエン酸デヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項１３】　配列番号３２に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ジヒドロリポアミドデヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

【請求項１４】　配列番号３４に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入

、付加、又は逆位を含むアミノ酸配列からなり、かつ、２－オキソグルタル酸デヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

【発明の詳細な説明】

【０００１】

【発明の属する技術分野】

本発明は、高温耐性コリネ型細菌であるコリネバクテリウム・サーモアミノゲネスの耐熱性酵素遺伝子、特にＬ－グルタミン酸等のＬ－アミノ酸生合成系酵素及び取り込み系遺伝子に関する。

【０００２】

【従来の技術】

現在、Ｌ－グルタミン酸等のＬ－アミノ酸の製造は、コリネ型細菌による発酵生産が主流となっている。アミノ酸の発酵生産は、生産能に優れた菌株の育種や発酵技術の開発によって、コストダウンが図られている。従来、コストダウン実現の方向性は、高収率化が主なものであるが、発酵におけるコストとしては、原料以外にも培養中に発生する発酵熱の冷却エネルギーを無視することはできない。すなわち、発酵に用いられている通常の微生物は、発酵中に自らが発生する発酵熱により培地の温度が上昇し、発酵に必要な酵素が失活したり生産菌が死滅したりするために、発酵中に培地を冷却することが必要となっている。したがって、冷却費用を低減するために、高温での発酵に関する検討が古くから行われている。また、高温で発酵を行うことが可能となれば、反応速度を向上させることができる可能性もある。しかし、これまでのところ、Ｌ－アミノ酸発酵において、有効な高温培養は実現していない。

【０００３】

コリネバクテリウム・サーモアミノゲネス（Corynebacterium thermoaminogenes）は、Ｌ－アミノ酸の発酵に汎用されているコリネバクテリウム・グルタミカム（C rynebacterium glutamicum）（ブレビバクテリウム・ラクトファーメンタム（Brevibacterium lactofermentum））等と同様にコリネ型細菌に分類される細菌であるが、生育至適温度はコリネバクテリウム・グルタミカムの30～35℃に対して37～43℃と高く、Ｌ－グルタミン酸生成の至適温度も42～45℃とかなり高

温側にシフトしている（特開昭６３－２４０７７９号）。

【０００４】

ところで、コリネバクテリウム属またはブレビバクテリウム属細菌において、エシェリヒア・コリ又はコリネバクテリウム・グルタミクム由来のＬ－アミノ酸合成系酵素をコードする遺伝子を導入することにより、同Ｌ－アミノ酸の生産能を増強する技術が開発されている。例えば、このような酵素として、例えば、Ｌ－グルタミン酸生合成系酵素であるクエン酸シンターゼ（特公平7-121228号）、グルタミン酸デヒドロゲナーゼ（特開昭61-268185号）、イソクエン酸デヒドロゲナーゼ、アコニット酸ヒドラターゼ遺伝子（特開昭63-214189号）等がある。

【０００５】

しかし、高温耐性のコリネ型細菌由来のＬ－アミノ酸生合成酵素及びそれらをコードする遺伝子は報告されていない。

【０００６】

【発明が解決しようとする課題】

本発明は、コリネバクテリウム・サーモアミノゲネス由来の酵素、好ましくはコリネバクテリウム・グルタミカムよりも高い温度で機能する酵素をコードする遺伝子を提供することを課題とする。

【０００７】

【課題を解決するための手段】

本発明者は、上記課題を解決するために鋭意検討を行った結果、コリネバクテリウム・サーモアミノゲネスのアミノ酸生合成系酵素をコードする遺伝子、又はアミノ酸の細胞内への取り込みに関与するタンパク質をコードする遺伝子を単離することに成功し、本発明を完成するに至った。

すなわち本発明は、以下のとおりである。

【０００８】

（ｉ）配列番号２に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソシトレートリアーゼ活性を有するタンパク質をコードするＤＮＡ。

（２）配列番号４に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アシルＣｏ－Ａカルボキシラーゼ活性に関与するタンパク質をコードするＤＮＡ。

（３）配列番号６に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ＤｔｓＲ活性を有するタンパク質をコードするＤＮＡ。

【０００９】

（４）配列番号８に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ＤｔｓＲ活性を有するタンパク質をコードするＤＮＡ。

（５）配列番号１０に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホフルクトキナーゼ活性を有するタンパク質をコードするＤＮＡ。

（６）配列番号１２又は１４に記載のアミノ酸配列、又は、前記アミノ酸配列のいずれかにおいて、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列を含み、かつ、インベルターゼ活性を有するタンパク質をコードするＤＮＡ。

【００１０】

（７）配列番号１７～２０に記載のアミノ酸配列のいずれかを有するタンパク質、又は、前記アミノ酸配列のいずれかにおいて、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、グルタミン酸の取り込みに関与する機能を有するタンパク質、をコードするＤＮＡ。

（８）配列番号２２に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸デヒドロゲナーゼ活性を有す

るタンパク質をコードするＤＮＡ。

（９）配列番号２４に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするＤＮＡ。

【００１１】

（１０）配列番号２６に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ホスホエノールピルビン酸カルボキシラーゼ活性を有するタンパク質をコードするＤＮＡ。

（１１）配列番号２８に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、アコニターゼ活性を有するタンパク質をコードするＤＮＡ。

（１２）配列番号３０に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、イソクエン酸デヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

【００１２】

（１３）配列番号３２に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、ジヒドロリポアミドデヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

（１４）配列番号３４に記載のアミノ酸配列を有するタンパク質、又は、同アミノ酸配列において、１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むアミノ酸配列からなり、かつ、２－オキソグルタル酸デヒドロゲナーゼ活性を有するタンパク質をコードするＤＮＡ。

【００１３】

以下、上記の各ＤＮＡのいずれか、又はこれらを総称して、本発明のＤＮＡと

いうことがある。

【００１４】

【発明の実施の形態】

以下、本発明を詳細に説明する。

本発明のＤＮＡの塩基配列及び遺伝子名、並びに本発明のＤＮＡがコードするタンパク質を以下に示す。

【００１５】

【表１】

表１

塩基配列	遺伝子名	コードされるタンパク質
配列番号１	aceA	イソシトレートリアーゼ
配列番号３	accBC	ｱｼﾙCo-AｶﾙﾎﾞｷｼﾗｰｾﾞBCサブユニット
配列番号５	dtsR1	ＤＴＳＲ１蛋白質
配列番号７	dtsR2	ＤＴＳＲ２蛋白質
配列番号９	pfk	ホスホフルクトキナーゼ
配列番号11,13,15	scrB	インベルターゼ
配列番号16	gluABCD	グルタミン酸取り込み系
配列番号21	pdhA	ピルビン酸デヒドロゲナーゼ
配列番号23	pc	ピルビン酸カルボキシラーゼ
配列番号25	ppc	ﾎｽﾎｴﾉｰﾙﾋﾟﾙﾋﾞﾝ酸ｶﾙﾎﾞｷｼﾗｰｾﾞ
配列番号27	acn	アコニターゼ
配列番号29	icd	イソクエン酸デヒドロゲナーゼ
配列番号31	lpd	ジヒドロリポアミドデヒドロゲナーゼ
配列番号33	odhA	２－オキソグルタル酸デヒドロゲナーゼ

【００１６】

尚、配列番号３、２３、２５、3-1及び3-3におけるオープン・リーディング・フレーム（ＯＲＦ）、及び配列番号１６の４番目のＯＲＦはいずれもGTGから始まっている。配列表にはこのGTGによりコードされるアミノ酸はバリンとして記載されているが、メチオニンである可能性がある。

【００１７】

また、配列番号16は４つのＯＲＦを含み、５’側から順にgluA、gluB、gluC及びgluDに対応する。

上記の各ＤＮＡは、コリネバクテリウム・サーモアミノゲネスAJ12310株（FERM BP-1542）の染色体ＤＮＡから単離されたものである。但し、AJ12310株は、インベルターゼ活性及びシュークロース資化性を持たず、同株から単離したscrB遺伝子断片には、オープンリーディングフレームが存在しなかったため、配列番号１１及び１３に示すＤＮＡは、インベルターゼ活性及びシュークロース資化性を有するコリネバクテリウム・サーモアミノゲネスAJ12340株（FERM BP-1539）及びAJ12309株（FERM BP-1541）からそれぞれ単離されたものである。

【００１８】

尚、配列番号１１、１３及び１５に示す塩基配列は、scrBの部分配列であって、配列番号１１及び１３は配列番号１２及び１４に示すインベルターゼの部分アミノ酸配列をコードしている。

【００１９】

目的とする遺伝子の部分断片を含むＤＮＡは、すでに報告されているブレビバクテリウム・ラクトファーメンタム等の種々の微生物の目的とする遺伝子の塩基配列の比較を行い、塩基配列がよく保存されている領域を選択し、その領域の塩基配列に基づいて設計したプライマーを用い、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡを鋳型とするＰＣＲを行うことによって、取得することができる。得られたＤＮＡ断片又はその配列に基づいて作製したプローブを用いたハイブリダイゼーションにより、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡライブラリーをスクリーニングすることによって、目的とする遺伝子全長を含むＤＮＡ断片を得ることができる。また、得られた遺伝子の部分断片を用いてゲノムウォーキングを行うことによっても、目的とする遺伝子全長を含むＤＮＡ断片を得ることができる。ゲノムウォーキングと、市販のキット、例えばTaKaRa LA PCR in vitro Cloning Kit（宝酒造（株）製）を用いて行うことができる。

【００２０】

また、本発明により、各遺伝子の塩基配列が明らかとなったので、それらの塩

基配列に基づいて作製したプライマーを用いたＰＣＲによって、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡ又は染色体ＤＮＡライブラリーから取得することもできる。

【００２１】

染色体ＤＮＡの調製、染色体ＤＮＡライブラリーの作製、ハイブリダイゼーション、ＰＣＲ、プラスミドＤＮＡの調製、ＤＮＡの切断及び連結、形質転換等の方法は、Sambrook,J.,Fritsch,E.F.,Maniatis,T.,Molecular Cloning, Cold Spring Harbor Laboratory Press,1.21(1989)に記載されている。

【００２２】

次に、本発明のＤＮＡを取得する具体的な方法を例示する。

まず、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡを、適当な制限酵素、例えばSau3AIで消化し、アガロースゲル電気泳動により分画して約4～6 kbのDNAフラグメントを取得する。得られたＤＮＡフラグメントをpHSG399等のクローニングベクターに挿入し、得られた組換えプラスミドでエシェリヒア・コリを形質転換して、染色体ＤＮＡのプラスミドライブラリーを作製する。

【００２３】

一方、プラスミドライブラリーから目的の遺伝子を含むクローンをＰＣＲにより選択するために用いるプライマーを作製する。このプライマーは、目的とする遺伝子に対応する種々の微生物の既知の遺伝子配列の間でアミノ酸レベルで保存されている領域に基づいて設計する。その際、コリネ型細菌のコドンユーセージを考慮してプライマーを複数組づつ設計する。

【００２４】

次に、作製されたプライマーの適正を調べるために、これらのプライマーを用いて、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡを鋳型としてＰＣＲを行う。そして、増幅断片が得られたプライマーをスクリーニング用プライマーとして用い、プラスミドライブラリーから調製した組換えプラスミドを鋳型としてＰＣＲを行い、目的とするＤＮＡ断片を含むクローンを選択する。この操作は、一次スクリーニングとして形質転換体数十株を含むバッチ毎に行い、二次スクリーニングとして増幅断片が得られたバッチについてコロニーＰＣＲを行う

ことにより、迅速に行うことができる。尚、増幅された遺伝子の断片長は、表２～７に記載した。

【００２５】

上記のようにして選択された形質転換体から組換えＤＮＡを調製し、挿入断片の塩基配列をダイ・デオキシ・ターミネーション法等により決定し、塩基配列を既知の遺伝子配列と比較することによって、目的の遺伝子を含むことを確認する。

【００２６】

得られたＤＮＡ断片が、目的とする遺伝子の一部を含んでいる場合には、ゲノムウォーキングにより欠失部分を取得する。

本発明のＤＮＡは、コードされるタンパク質が本来の機能を有する限り、１若しくは複数の位置での１若しくは数個のアミノ酸の置換、欠失、挿入、付加、又は逆位を含むタンパク質をコードするものであってもよい。ここで、「数個」とは、アミノ酸残基のタンパク質の立体構造における位置や種類によっても異なるが、一般的に、それぞれのタンパク質のアミノ酸配列全体に対し、３０から４０％以上、好ましくは５５～６５％以上の相同性を有することが好ましい。具体的には、前記「数個」は、２～数百個、好ましくは、２～数十個、より好ましくは２～１０個である。

【００２７】

上記のような本来のタンパク質と実質的に同一のタンパク質をコードするＤＮＡは、例えば部位特異的変異法によって、特定の部位のアミノ酸残基が置換、欠失、挿入、付加、又は逆位を含むように、それぞれのタンパク質をコードするＤＮＡの塩基配列を改変することによって得られる。また、上記のような改変されたＤＮＡは、従来知られている変異処理によっても取得され得る。変異処理としては、目的の遺伝子をコードするＤＮＡをヒドロキシルアミン等でインビトロ処理する方法、及び目的の遺伝子をコードするＤＮＡを保持する微生物、例えばエシェリヒア属細菌を、紫外線照射またはN－メチル－N'－ニトロ－N－ニトロソグアニジン（NTG）もしくは亜硝酸等の通常変異処理に用いられている変異剤によって処理する方法が挙げられる。

【００２８】

また、上記のような塩基の置換、欠失、挿入、付加、又は逆位等には、コリネバクテリウム・サーモアミノゲネスの菌株の違い等に基づく場合などの天然に生じる変異（mutant又はvariant）も含まれる。

【００２９】

変異を有するＤＮＡを、適当な細胞で発現させ、発現産物のタンパク質の活性又は機能を調べることにより、本来のタンパク質と実質的に同一のタンパク質をコードするＤＮＡが得られる。また、そのようなＤＮＡは、変異を有するタンパク質をコードするＤＮＡまたはこれを保持する細胞から、例えば表１に示す各配列番号の塩基配列を有するＤＮＡ又はその塩基配列から調製されるプローブとストリンジェントな条件下でハイブリダイズし、かつ、当該タンパク質が本来有する活性を示すタンパク質をコードするＤＮＡを単離することによっても得ることができる。

【００３０】

上記プローブは、表１に示す各配列番号の塩基配列を有するＤＮＡ、又はそれらの塩基配列を有するＤＮＡから、適当なプライマーを用いてＰＣＲにより調製することができる。

【００３１】

上記でいう「ストリンジェントな条件」とは、いわゆる特異的なハイブリッドが形成され、非特異的なハイブリッドが形成されない条件をいう。この条件を明確に数値化することは困難であるが、一例を示せば、相同性が高いＤＮＡ同士、例えば５０％以上の相同性を有するＤＮＡ同士がハイブリダイズし、それより相同性が低いＤＮＡ同士がハイブリダイズしない条件、あるいは通常のサザンハイブリダイゼーションの洗いの条件である６０℃、１×ＳＳＣ，０．１％ＳＤＳ、好ましくは、０．１×ＳＳＣ、０．１％ＳＤＳに相当する塩濃度でハイブリダイズする条件が挙げられる。

【００３２】

このような条件でハイブリダイズする遺伝子の中には途中にストップコドンが発生したものや、活性中心の変異により活性を失ったものも含まれるが、それら

については、市販の活性発現ベクターにつなぎ、活性又は機能を調べることによって容易に取り除くことができる。

【００３３】

本発明のＤＮＡを、適当な宿主－ベクター系を用いて発現させることにより、それぞれのＤＮＡに対応したタンパク質を製造することができる。

遺伝子の発現に用いる宿主としては、ブレビバクテリウム・ラクトファーメンタム（コリネバクテリウム・グルタミカム）、コリネバクテリウム・サーモアミノゲネス等のコリネ型細菌、エシェリヒア・コリ、バチルス・ズブチリスをはじめとする種々の原核細胞、サッカロマイセス・セレビシエ（Saccharomyces cerevisiae）をはじめとする種々の真核細胞、動物細胞、植物細胞が挙げられるが、これらの中では原核細胞、特にコリネ型細菌及びエシェリヒア・コリが好ましい。

【００３４】

本発明のＤＮＡは、エシェリヒア・コリ及び／又はコリネ型細菌等の細胞内において自律複製可能なベクターＤＮＡに接続して組換えＤＮＡを調製し、これをエシェリヒア・コリ細胞に導入しておくと、後の操作がしやすくなる。エシェリヒア・コリ細胞内において自律複製可能なベクターとしては、プラスミドベクターが好ましく、宿主の細胞内で自立複製可能なものが好ましく、例えば pUC19、pUC18、pBR322、pHSG299、pHSG399、pHSG398、RSF1010等が挙げられる。

【００３５】

コリネ型細菌の細胞内において自律複製可能なベクターとしては、pAM330（特開昭58-67699号公報参照）、pHM1519（特開昭58-77895号公報参照）等が挙げられる。また、これらのベクターからコリネ型細菌中でプラスミドを自律複製可能にする能力を持つＤＮＡ断片を取り出し、前記エシェリヒア・コリ用のベクターに挿入すると、エシェリヒア・コリ及びコリネ型細菌の両方で自律複製可能ないわゆるシャトルベクターとして使用することができる。

【００３６】

このようなシャトルベクターとしては、以下のものが挙げられる。尚、それぞれのベクターを保持する微生物及び国際寄託機関の受託番号をかっこ内に示した

pAJ655　エシェリヒア・コリAJ11882(FERM BP-136)

コリネバクテリウム・グルタミクムSR8201(ATCC39135)

pAJ1844 エシェリヒア・コリAJ11883(FERM BP-137)

コリネバクテリウム・グルタミクムSR8202(ATCC39136)

pAJ611　エシェリヒア・コリAJ11884(FERM BP-138)

pAJ3148 コリネバクテリウム・グルタミクムSR8203(ATCC39137)

pAJ440　バチルス・ズブチリスAJ11901(FERM BP-140)

pHC4　エシェリヒア・コリAJ12617(FERM BP-3532)

【００３７】

本発明のＤＮＡとコリネ型細菌で機能するベクターを連結して組み換えＤＮＡを調製するには、本発明のＤＮＡの末端に合うような制限酵素でベクターを切断する。連結は、Ｔ４ＤＮＡリガーゼ等のリガーゼを用いて行うのが普通である。

【００３８】

上記のように調製した組み換えＤＮＡをコリネ型細菌等の宿主に導入するには、これまでに報告されている形質転換法に従って行えばよい。例えば、エシェリヒア・コリ　Ｋ－１２について報告されているような、受容菌細胞を塩化カルシウムで処理してＤＮＡの透過性を増す方法（Mandel,M.and Higa,A.,J. Mol. Biol., 53, 159 (1970)）があり、バチルス・ズブチリスについて報告されているような、増殖段階の細胞からコンピテントセルを調製してＤＮＡを導入する方法（Duncan,C.H.,Wilson,G.A.and Young,F.E., Gene, 1, 153 (1977)）がある。あるいは、バチルス・ズブチリス、放線菌類及び酵母について知られているような、ＤＮＡ受容菌の細胞を、組換えＤＮＡを容易に取り込むプロトプラストまたはスフェロプラストの状態にして組換えＤＮＡをＤＮＡ受容菌に導入する方法（Chang,S.and Choen,S.N.,Molec. Gen. Genet., 168, 111 (1979);Bibb,M.J.,Ward,J.M.and Hopwo d,O.A.,Nature, 274, 398 (1978);Hinnen,A.,Hicks,J.B.and Fink,G.R.,Proc. Natl. Acad. Sci. USA, 75 1929 (1978)）も応用できる。コリネ型細菌においては、電気パルス法（特開平２－２０７７９１号公報参照）が有効である。

【００３９】

本発明のＤＮＡに含まれる遺伝子の発現を効率的に実施するために、これらの遺伝子のコード領域の上流に、宿主細胞内で働くｌａｃ、ｔｒｐ、P_L等のプロモーターを連結してもよい。ベクターとして、プロモーターを含むベクターを用いると、各遺伝子と、ベクター及びプロモーターとの連結を一度に行うことができる。

【００４０】

上記のようにして製造されるタンパク質は、必要に応じて、菌体抽出液又は培地からイオン交換クロマトグラフィー、ゲル濾過クロマトグラフィー、吸着クロマトグラフィー、塩析、溶媒沈殿等、通常の酵素の精製法を用いて精製することができる。

【００４１】

本発明のＤＮＡのうち、pfk、pdhA、pc、ppc、acn及びicdは、コリネ型細菌等のＬ－アミノ酸生産菌に導入することによって、Ｌ－アミノ酸生産能を高めることができる。また、本発明のＤＮＡが導入されたコリネ型細菌は、通常よりも高い温度でのＬ－アミノ酸の生産が可能となることが期待される。Ｌ－アミノ酸としては、Ｌ－グルタミン酸、Ｌ－アスパラギン酸、Ｌ－リジン、Ｌ－アルギニン、Ｌ－プロリン及びＬ－グルタミン等が挙げられる。

【００４２】

また、dtsR1及びdtsR2は、コリネ型細菌に界面活性剤に対する耐性を付与する蛋白質（ＤＴＳＲ蛋白）をコードする遺伝子であり、これらの遺伝子が破壊されたコリネ型Ｌ－グルタミン酸生産菌は、野生株がほとんどＬ－グルタミン酸を生成しない量のビオチンが存在する条件においても著量のＬ－グルタミン酸を生成する。また、Ｌ－リジン生産能を有するコリネ型Ｌ－グルタミン酸生産菌は、dtsR1及びdtsR2遺伝子を増幅すると、著量のＬ－リジンを生産する能力が付与される（WO95/23224号国際公開パンフレット、特願平10-234371号公報）。

【００４３】

scrB遺伝子は、シュークロースを含む培地でコリネ型細菌を用いてＬ－アミノ酸を製造する場合に、同コリネ型細菌の育種に用いることができる。

コリネ型細菌等のＬ－グルタミン酸生産菌において、のaceA、accBC、lpd又はodhAを欠失させることにより、Ｌ－グルタミン酸生産性を高めることができる。また、gluABCDはＬ－グルタミン酸の取り込み系の遺伝子クラスターであり、コリネ型Ｌ－グルタミン酸生産菌において、gluA、gluB、gluCもしくはgluD、又はこれらの１種、２種、３種もしくは４種を欠失させることにより、培地に蓄積されるＬ－グルタミン酸量を増大させることができる。本発明のaceA、accBC、lpd、odhA及びgluABCDは、染色体上のこれらの遺伝子を破壊するのに用いることができる。

【００４４】

【実施例】

以下、本発明を実施例によりさらに具体的に説明する。

【００４５】

＜１＞コリネバクテリウム・サーモアミノゲネスのプラスミドライブラリーの作製

コリネバクテリウム・サーモアミノゲネス AJ12310株を、CM2B液体培地（イーストエキストラクト（Difco社製）1g/dl、ポリペプトン（日本製薬製）1g/dl、NaCl 0.5g/dl、ビオチン 10μg/dl、pH 7.0（KOHで調整））で37℃にて15時間培養し、10mlの培養液から、染色体DNAを染色体DNA抽出キット（Bacterial Genome DNA Purification Kit（Advanced Genetic Technologies社製）を用いて取得した。取得したDNAを、制限酵素Sau3AIを用いて部分消化し、0.8%アガロースゲル電気泳動を行い、DNAを分画した後に、約4～6kbのDNAフラグメントをゲルから切り出し、DNAゲル抽出キット（GIBCO BRL社、Concert^{TM}Rapid Gel Extraction System）を用いて、目的サイズのDNA断片を取得した。

【００４６】

プラスミドpHSG399（宝酒造（株）製）をBamHIで完全消化し、末端をアルカリフォスファターゼ（CIAP；宝酒造（株）製）を用いて脱リン酸化した。このベクター断片と、上記の染色体DNA断片を宝酒造社製DNAライゲーションキットを用いて連結し、得られた組換えベクターを用いてエシェリヒア・コリ JM109を形質転換した。形質転換体の選択は、30μg/mlのクロラムフェニコール、0.04mg/mlのI

PTG（イソプロピル－β－Ｄ－チオガラクトピラノシド）、0.04mg/mlのX-Gal（５－ブロモ－４－クロロ－３－インドリル－β－Ｄ－ガラクトシド）を含むLB寒天培地（寒天 1.5g/dlを含む）上にて行い、白色コロニーを約4000コロニー取得した。

【００４７】

＜２＞各遺伝子断片増幅用プライマーの設定

上記で得られたプラスミドライブラリーから目的の遺伝子を含むクローンをＰ.C.Ｒにより選択するために用いるプライマーを設計した。目的とする遺伝子は前記のとおりである。

【００４８】

プライマーは、コリネ型細菌の既知の遺伝子配列をベースとして、他の微生物の相当する遺伝子との間でアミノ酸レベルで保存されている領域に基づいて設計した。その際、コリネ型細菌のコドンユーセージを考慮してプライマーを複数組づつ設計した。

【００４９】

作製されたプライマーの適正を調べるために、これらのプライマーを用いて、コリネバクテリウム・サーモアミノゲネスAJ12310株の染色体ＤＮＡを鋳型としてＰＣＲを行い、遺伝子断片を増幅した。その結果、いずれの遺伝子も、表２～表７の上段に示すプライマーを用い、各表中に「部分断片取得のPCR」として示した条件及びポリメラーゼでＰＣＲを行った場合に、増幅断片が認められた。各プライマーの末尾のカッコ内の数字は、配列表中の配列番号を示す。これらのプライマーを、後述のスクリーニング用プライマーとして用いた。

【００５０】

【表２】

表２

遺伝子名	aceA	accBC	dtsRI
5'→3'ﾌﾟﾗｲﾏｰ 3'→5'ﾌﾟﾗｲﾏｰ	CCTCTACCCAGCGAACTCCG (35) CTGCCTTGAACTCACGGTTC (36)	CATCCACCCCGGCTACGGCT (37) CGGTGACTGGGTGTTCCACC (38)	ACGGCCCAGCCCTGACCGAC (39) AGCAGCGCCCATGACGGCGA (40)
部分断片取得のPCR条件 及び ｽｸﾘｰﾆﾝｸﾞPCRの条件	94℃ 5min 98℃ 5sec 66℃ 2sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 66℃ 2sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 66℃ 2sec 30 cycle Z-Taq
ｺﾛﾆｰ-PCRの条件	94℃ 7min 91℃ 30sec 55℃ 1sec 72℃ 2.5min 30 cycle Ex-Taq	94℃ 7min 91℃ 30sec 55℃ 1sec 72℃ 2.5min 30 cycle Ex-Taq	94℃ 7min 91℃ 30sec 55℃ 1sec 72℃ 2.5min 30 cycle Ex-Taq
増幅断片	824bp	673bp	805bp

【００５１】

【表３】

表３

遺伝子名	dtsR2	pfk	scrB
5'→3'ﾌﾟﾗｲﾏｰ 3'→5'ﾌﾟﾗｲﾏｰ	ACGGCCCAGCCCTGACCGAC (41) AGCAGCGCCCATGACGGCGA (42)	CGTCATCCGAGGAATCGTCC (43) CGTGGCGGGCCATGACCTCC (44)	GGNCGHYTBAAYGAYCC (45) GGRCAYTCCCACATRTANCC (46)
部分断片取得のPCR条件！及び ｽｸﾘｰﾆﾝｸﾞPCRの条件	94℃ 5min 98℃ 5sec 66℃ 2sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 66℃ 2sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 50℃ 10sec 72℃ 20sec 40 cycle Z-Taq
ｺﾛﾆｰPCRの条件	94℃ 7min 91℃ 30sec 55℃ 1sec 72℃ 2.5min 30 cycle Ex-Taq	94℃ 7min 91℃ 30sec 55℃ 1sec 72℃ 2.5min 30 cycle Ex-Taq	94℃ 7min 91℃ 30sec 55℃ 1sec 72℃ 2.5min 30 cycle Ex-Taq
増幅断片	805bp	472bp	500bp

【００５２】

【表４】

表４

遺伝子名	gluABCD	pdhA
5'→3'ﾌﾟﾗｲﾏｰ 3'→5'ﾌﾟﾗｲﾏｰ	CCATCCGGATCCGGCAAGTC (47) AATCCCATCTCGTGGGTAAC (48)	ACTGTGTCCATGGGTCTTGGCCC (49) CGCTGGAATCCGAACATCGA (50)
部分断片取得のPCR条件	94℃ 5min 98℃ 5sec 50℃ 10sec 72℃ 20sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 50℃ 10sec 72℃ 20sec 30 cycle Z-Taq
増幅断片	500bp	1200bp
ｽｸﾘｰﾆﾝｸﾞPCR ｺﾛﾆｰPCRの条件	94℃ 5min 94℃ 30sec 50℃ 1min 72℃ 2min 30 cycle EX-Taq	94℃ 5min 94℃ 30sec 50℃ 1min 72℃ 2min 30 cycle EX-Taq

【００５３】

【表５】

表５

遺伝子名	pc	ppc
5'→3'ﾌﾟﾗｲﾏｰ 3'→5'ﾌﾟﾗｲﾏｰ	GGCGCAACCTACGACGTTGCAATGCG (51) TGGCCGCCTGGGATCTCGTG (52)	GGTTCCTGGATTGGTGGAGA (53) CCGCCATCCTTGTTGGAATC (54)
部分断片取得のPCR条件	94℃, 5min 98℃, 5sec 55℃, 80sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 50℃ 5sec 72℃ 10sec 30 cycle Z-Taq
増幅断片	781bp	1000bp
ｽｸﾘｰﾆﾝｸﾞPCRの条件	94℃, 5min 98℃, 5sec 55℃, 80sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 50℃ 5sec 72℃ 10sec 30 cycle Z-Taq
ｺﾛﾆｰPCRの条件	94℃, 5min 1 cycle 98℃, 5sec 55℃, 80sec 50 cycle Z-Taq	94℃ 5min 98℃ 5sec 50℃ 10sec 72℃ 20sec 50 cycle Z-Taq

【００５４】

【表６】

表6

遺伝子名	acn	icd	lpd
5'→3' ﾌﾟﾗｲﾏｰ 3'→5' ﾌﾟﾗｲﾏｰ	GTIGGIACIGAYTCSCATAC (55) GCIGGAGAIATGTGRTCIGT (56)	GACATTTCACTCGCTGGACG (57) CCGTACTCTTCAGCCTTCTG (58)	ATCATCGCAACCGGTTC (59) CGTCACCGATGGCGTAAAT (60)
部分断片 取得の PCR条件	94℃ 1min 96℃ 20sec 45℃ 1min 68℃ 2min 30 cycle EX-Taq	94℃ 5min 98℃ 5sec 55℃ 80sec 30 cycle Z-Taq	94℃ 5min 98℃ 5sec 50℃ 10sec 72℃ 20sec 30 cycle Z-Taq
増幅断片	1500bp	1500bp	500bp
ｽｸﾘｰﾆﾝｸﾞPCR ﾌﾛﾆｰPCR の条件	同 上	同 上	94℃ 5min 94℃ 30sec 57℃ 1min 72℃ 1min 30 cycle Ex-Taq
ｽｸﾘｰﾆﾝｸﾞPCR 5'→3' ﾌﾟﾗｲﾏｰ 3'→5' ﾌﾟﾗｲﾏｰ			TACGAGGAGCAGATCCTCAA (63) TTGACGCCGGTGTTCTCCAG (64)
LAｸﾛｰﾆﾝｸﾞ(N')	S1:GGTGAAGCTAAGTAGTTAGC (65)	S1:CCGTACTCTTCAGCCTTCTG (67)	S1:ATCATCGCAACCGGTTC (69)
3'→5' ﾌﾟﾗｲﾏｰ	S2:AGCTACTAAACCTGCACC (66)	S2:TCGTCCTTGTTCCACATC (68)	S2:TACGAGGAGCAGATCCTCAA (70)
LAｸﾛｰﾆﾝｸﾞ(C')	S1:GCTAACTACTTAGCTTCACC (71)	S1:TCCGATGTCATCATCGAC (73)	
5'→3' ﾌﾟﾗｲﾏｰ	S2:GAACCAGGAACTATTGAACC (72)	S2:ATGTGGAACAAGGACGAC (74)	
制限酵素	PstI(N') HindIII(C')	SalI(N') PstI(C')	HindIII
LAｸﾛｰﾆﾝｸﾞ の条件	N' 94℃ 1min 94℃ 30sec 57℃ 2min 72℃ 2min 30 cycle LA-Taq C' 94℃ 1min 94℃ 30sec 57℃ 2min 72℃ 2.5min 30 cycle LA-Taq	94℃ 1min 94℃ 30sec 57℃ 2min 72℃ 2.5min 30 cycle LA-Taq	94℃ 1min 94℃ 30sec 57℃ 2min 72℃ 1min 30 cycle LA-Taq

【００５５】

【表７】

表７

遺伝子名	odhA
5'→3'ﾌﾟﾗｲﾏｰ 3'→5'ﾌﾟﾗｲﾏｰ	ACACCGTGGTCGCCTCAACG (61) TGCTAACCCGTCCCACCTGG (62)
部分断片取得のPCR条件	94℃ 5min 98℃ 5sec 66℃ 2sec 30 cycle Z-Taq
増幅断片	1306bp
LAｸﾛｰﾆﾝｸﾞ（N'） 5'→3'ﾌﾟﾗｲﾏｰ	S1:GTACATATTGTCGTTAGAACGCGTAATACGACTCA (75) S2:CGTTAGAACGCGTAATACGACTCACTATAGGGAGA (76)
制限酵素	XbaI
LAｸﾛｰﾆﾝｸﾞﾟの条件	１回目 94℃ 30seC 55℃ 2min 72℃ 1min 30cycle LA-Taq ２回目 94℃ 1min 98℃ 20seC 68℃ 15min 30 cycle 72℃ 10min LA-Taq

＜３＞ＰＣＲによるプラスミドライブラリーのスクリーニング

前記のプラスミドライブラリーから目的の遺伝子を含むクローンを、ＰＣＲにより選択した。プラスミドライブラリーから、コロニーを６０個ずつピックアップし、２枚づつのLB寒天培地プレートにレプリカした。各プレートのコロニー６０個づつをまとめて、4mlのLB液体培地を含む試験管に接種し、15時間培養した後、プロメガ社製プラスミドDNA抽出キットを用いてそれぞれプラスミドの混合物を取得した。このプラスミド混合物を鋳型とし、各目的遺伝子毎に作製したスクリーニング用プライマーを用いて、各表中に「スクリーニングPCRの条件」として示した条件でＰＣＲを行い、染色体ＤＮＡを鋳型とするＰＣＲと同じ大きさ

のDNA断片が増幅されるクローンを選択した。

【００５６】

増幅されたDNA断片は、パーキンエルマー社製ビッグダイ・ダイターミネーターサイクルシークエンスキットを用いて塩基配列を決定し、既知の遺伝子情報との相同性を比較することにより、目的遺伝子の取得の成否を確認した。

【００５７】

尚、１ｐｄについては、＜２＞で作製したプライマーでは目的のＤＮＡ断片が増幅されなかったので、決定された塩基配列に基づいて、スクリーニング用プライマーを別途作製した。

【００５８】

＜４＞コロニーＰＣＲによる目的遺伝子保持クローンの選択

目的の遺伝子断片の増幅が確認されたプラスミド混合物が由来するプレートを用いて、コロニーＰＣＲを行い、遺伝子断片を含むクローンを選択した。コロニーＰＣＲは、表２～７に示す条件で行った。

【００５９】

選択された形質転換体からプラスミドＤＮＡを回収し、挿入ＤＮＡ断片の塩基配列を決定した。挿入ＤＮＡ断片に目的遺伝子の全長が挿入されておらず、遺伝子の上流域、下流域またはこれらの両方が欠失している場合は、判明した塩基配列を利用してプライマーを作製し、TaKaRa LA PCR in vitro Cloning Kit（宝酒造（株））を用いて、目的遺伝子の全領域の遺伝子断片を取得し、塩基配列を決定した。

【００６０】

LA PCRクローニングの概要は以下のとおりである。挿入ＤＮＡ断片のうち２つの領域の塩基配列を有する２種のプライマーを作製する。コリネバクテリウム・サーモアミノゲネスAJ12310株の染色体ＤＮＡを各種制限酵素で切断し、各制限酵素に対応したカセットプライマーと連結する。これを鋳型として、作製されたプライマーのうち欠失部分から遠い位置に対応するプライマー（Ｓ１）と、カセットプライマーの外側の位置に対応するカセットプライマー（Ｃ１）を用いてＰＣＲを行う。次に、作製されたプライマーのうち欠失部分に近い位置に対応する

プライマー（Ｓ２）と、カセットプライマーの内側の位置に対応するカセットプライマー（Ｃ２）を用いてＰＣＲを行う。こうして、欠失部分を含むＤＮＡ断片が得られる。得られたＤＮＡ断片と既に取得されいるＤＮＡ断片を連結することにより、目的遺伝子全長を含むＤＮＡ断片を得ることができる。尚、カセットの５’末端にはリン酸基が付いていないので、ＤＮＡ断片の３’末端とカセットの５’末端との接続部位にはニックができる。そのため、１回目のＰＣＲではプライマーＣ１からのＤＮＡ合成はこの接続部分でストップし、非特異的な増幅は起こらないため、特異的な増幅を行うことができる。

【００６１】

LA PCRクローニングに用いたプライマーと反応条件は、表２～７に示した。表中「(N')」は上流側の欠失部分のクローニングに用いたプライマーを、「(C')」は下流側の欠失部分のクローニングに用いたプライマーを、それぞれ示す。また、ＰＣＲ反応はLA PCRクローニングキットの説明書に従い、２回行った。表に示したプライマーのうち、上段には１回目の反応に用いたプライマー（Ｓ１）を、下段には２回目の反応に用いたプライマー（Ｓ２）を示す。

【００６２】

上記のようにして得られた各遺伝子を含むＤＮＡ断片の塩基配列を、前記と同様にして決定した。それらの塩基配列及び同塩基配列がコードし得るアミノ酸配列を、配列番号１～３４に示す。各配列番号に記載された配列は、下記のとおりである。

【００６３】

scrBについては、オープン・リーディング・フレームが見つからなかった。コリネバクテリウム・サーモアミノゲネス AJ12310株は、インベルターゼ活性を有しておらず、シュークロース資化性を持たないため、シュークロース資化性を有するコリネバクテリウム・サーモアミノゲネス YS-40株及びYS-155株から、同様にしてscrB遺伝子断片を取得した。その結果、いずれの株からもオープン・リーディング・フレームを有するＤＮＡ断片が得られた。

【００６４】

配列番号１： aceA　塩基配列

配列番号２： aceA　アミノ酸配列
配列番号３： accBC　塩基配列
配列番号４： accBC　アミノ酸配列
配列番号５： dtsR1　塩基配列
配列番号６： dtsR1　アミノ酸配列
配列番号７： dtsR2　塩基配列
配列番号８： dtsR2　アミノ酸配列
配列番号９： pfk　塩基配列
配列番号10： pfk　アミノ酸配列
配列番号11： scrB　塩基配列
配列番号12： scrB　アミノ酸配列
配列番号13： scrB　塩基配列
配列番号14： scrB　アミノ酸配列
配列番号15： scrB　塩基配列
配列番号16： gluABCD塩基配列
配列番号17： gluABCDアミノ酸配列
配列番号18： gluABCDアミノ酸配列
配列番号19： gluABCDアミノ酸配列
配列番号20： gluABCDアミノ酸配列
配列番号21： pdhA　塩基配列
配列番号22： pdhA　アミノ酸配列
配列番号23： pc　塩基配列
配列番号24： pc　アミノ酸配列
配列番号25： ppc　塩基配列
配列番号26： ppc　アミノ酸配列
配列番号27： acn　塩基配列
配列番号28： acn　アミノ酸配列
配列番号29： icd　塩基配列
配列番号30： icd　アミノ酸配列

配列番号31： lpd　塩基配列

配列番号32： lpd　アミノ酸配列

配列番号33： odhA　塩基配列

配列番号34： odhA　アミノ酸配列

【００６５】

【発明の効果】

本発明により、コリネバクテリウム・サーモアミノゲネスのアミノ酸生合成系酵素をコードする遺伝子、又はアミノ酸の細胞内への取り込みに関与するタンパク質をコードする遺伝子が提供される。

本発明の遺伝子は、前記酵素又はタンパク質の製造、又はアミノ酸生産菌の育種に利用することができる。

【００６６】

【配列表】

SEQUENCE LISTING

<110> Ajinomoto, Co., Inc.

<120> 高温耐性コリネ型細菌の耐熱性アミノ酸生合成系酵素遺伝子

<130> P-6910

<140>

<141> 1999-11-01

<160> 76

<170> PatentIn Ver. 2.0

【００６７】

<210> 1

<211> 1980

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (577)..(1869)

<400> 1

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atgcaaagct ccttcgaagc aagagatcgg gtgtgtgcgg gcacctatcg ggggaagccc 120

tcgctgcgcc ccaggggggag ctggcgatgt gaccaggtta agtgataacc atcaccttgc 180

caatgggttt gcgaacttta ccgtgacgct acccccgctt ttgtttgatc acaccagctc 240

gaaggctgtc gcttttccga agatgcacgt gaagtggcaa atccttgcca cccgaggttt 300

tcccagtaca aacgtactag tgatgaggat cacggggaac attgtggaga ttgcactttg 360

caatatttgc aaaaggggtg actacccccg cgcaaaactt aaaaacccaa atccgttgac 420

ggacccatgc ccgatgaagc aatgtgtgaa gcacgccacc ggaacacagg ttgtggatca 480

ctcaccatga tgtgggggat tcgcatcaca cagtgtgcag ggcggcacct ctaccgaatg 540

cgccttacag cagcaccaag aagaagtgac tcttag atg tca aac gtt gga acg 594

Met Ser Asn Val Gly Thr

1 5

cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cca cgc 642

Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro Arg

10 15 20

tgg aac gga atc acc cgc gac tac acc gct gag cag gta gct gag ctc 690

Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Glu Gln Val Ala Glu Leu

25 30 35

cag ggc agc gtc gtc gag gag cac acc ctc gca aag cgc ggc gcc gag 738

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Gln Gly Ser Val Val Glu Glu His Thr Leu Ala Lys Arg Gly Ala Glu
     40                  45                  50
atc ctg tgg gat gca gtt tcc gca gag ggc gac gac tac atc aac gca   786
Ile Leu Trp Asp Ala Val Ser Ala Glu Gly Asp Asp Tyr Ile Asn Ala
 55                  60                  65                  70
ctg ggc gcc ctt acc ggt aac cag gct gtc cag cag gtc cgt gcc ggc   834
Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala Gly
                 75                  80                  85
ctg aag gct gtc tac ctc tcc ggc tgg cag gtc gca ggt gac gcc aac   882
Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala Asn
             90                  95                 100
ctc gcc ggt cac acc tac ccc gac cag tcc ctg tac ccg gcg aac tcc   930
Leu Ala Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn Ser
        105                 110                 115
gtc ccg aac gtt gtc cgt cgc atc aac aac gca ctg ctg cgc gcc gat   978
Val Pro Asn Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ala Asp
    120                 125                 130
gag atc gca cgc gtc gag ggt gac acc tcc gtc gac aac tgg ctc gtc   1026
Glu Ile Ala Arg Val Glu Gly Asp Thr Ser Val Asp Asn Trp Leu Val
135                 140                 145                 150
ccg atc gtc gcc gac ggc gag gcc ggc ttc ggt ggc gcc ctc aac gtc   1074
Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn Val
                155                 160                 165
tac gag ctc cag aag ggc atg atc acc gct ggt gcc gca ggc acc cac   1122
Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala Gly Ala Ala Gly Thr His
            170                 175                 180
tgg gag gat cag ctc gct tcc gag aag aag tgt ggc cac ctc ggt ggc   1170
Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly Gly
        185                 190                 195
```

aag gtc ctc atc ccg acc cag cag cac atc cgc acc ctg aac tcc gcc 1218
Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser Ala
200 205 210

cgc ctg gca gct gac gtg gcc aac acc ccg acc gtc gtc atc gcc cgc 1266
Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala Arg
215 220 225 230

acc gac gca gag gcc gcc acc ctg atc acc tct gat gtt gat gag cgc 1314
Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu Arg
235 240 245

gac cgc cca ttc atc acc ggc gag cgc acc gcc gag ggc tac tac cac 1362
Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr His
250 255 260

gtc aag ccg ggt ctc gag ccc tgc atc gca cgt gcg aag tcc tac gct 1410
Val Lys Pro Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr Ala
265 270 275

ccc tac gca gac atg atc tgg atg gag acc ggc acc cct gac ctc gag 1458
Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu Glu
280 285 290

ctg gcc aag aag ttc gcc gag ggc gtc cgc agc gag ttc ccg gac cag 1506
Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp Gln
295 300 305 310

ctg ctg tcc tac aac tgc tcc ccg tcc ttc aac tgg tct gca cac ctc 1554
Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His Leu
315 320 325

gag gcc gac gag atc gct aag ttc cag aag gaa ctg ggt gcc atg ggc 1602
Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met Gly
330 335 340

ttc aag ttc cag ttc atc acc ctg gct ggc ttc cac tcc ctc aac tac 1650
Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn Tyr

```
        345                 350                 355
ggt atg ttc gac ctg gct tac ggc tac gcc cgt gaa ggc atg ccc gcc   1698
Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Pro Ala
    360                 365                 370
ttc gtc gac ctg cag aac cgt gag ttc aag gca gct gag gag cgc ggc   1746
Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg Gly
375                 380                 385                 390
ttc acc gcc gtc aag cac cag cgt gag gtc ggc gcc ggc tac ttc gac   1794
Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe Asp
                395                 400                 405
acc atc gcc acc acc gtt gac ccg aac tcc tcc acc acc gcg ctg aag   1842
Thr Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu Lys
            410                 415                 420
ggt tcc acc gag gaa tgc cag ttc cac taggaaccac ctgatgcggt         1889
Gly Ser Thr Glu Glu Cys Gln Phe His
        425                 430
gccgtatggc ctgacggcac cgcccctccc tttgcactcc agtactcctt tgtgcacatc 1949
ggccatctcc acaccgcgcg ccccgccacc t                                1980
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【００６８】

<210> 2

<211> 431

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 2

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Met Ser Asn Val Gly Thr Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
 1               5                  10                  15
Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
            20                  25                  30
```

Glu Gln Val Ala Glu Leu Gln Gly Ser Val Val Glu Glu His Thr Leu
35 40 45
Ala Lys Arg Gly Ala Glu Ile Leu Trp Asp Ala Val Ser Ala Glu Gly
50 55 60
Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
65 70 75 80
Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
85 90 95
Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
100 105 110
Leu Tyr Pro Ala Asn Ser Val Pro Asn Val Val Arg Arg Ile Asn Asn
115 120 125
Ala Leu Leu Arg Ala Asp Glu Ile Ala Arg Val Glu Gly Asp Thr Ser
130 135 140
Val Asp Asn Trp Leu Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
145 150 155 160
Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala
165 170 175
Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
180 185 190
Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
195 200 205
Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
210 215 220
Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
225 230 235 240
Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr
245 250 255
Ala Glu Gly Tyr Tyr His Val Lys Pr Gly Leu Glu Pr Cys Ile Ala

260 265 270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Il Trp Met Glu Thr

275 280 285

Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg

290 295 300

Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe

305 310 315 320

Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys

325 330 335

Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly

340 345 350

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala

355 360 365

Arg Glu Gly Met Pro Ala Phe Val Asp Leu Gln Asn Arg Glu Phe Lys

370 375 380

Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val

385 390 395 400

Gly Ala Gly Tyr Phe Asp Thr Ile Ala Thr Thr Val Asp Pro Asn Ser

405 410 415

Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Cys Gln Phe His

420 425 430

【００６９】

<210> 3

<211> 2384

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (577)..(2352)

<400> 3

agcaggccgt gttgccgaac ggcaacttcc gcagccgcaa ggagatcgag gaggtgtact 60

cgcacctcaa ccctgccgag gacaccgtgg tgtactgccg cgtgggtgac cgcgcggccc 120

acacctggtt cgtgttgaag tacctgctgg ggtttgaaaa cgtccgcaac tatgacggtt 180

cctggtccga gtggggcaac atggtgcgca tgcccatcgt ccagggtgat gagccgggct 240

cactctagtc accccggggt cacctccctg gtcacccccg taccctcccg ggtacacccc 300

ggggacgggg tgtgacctgg atctcccctg catgtggaca ccgggaaact ttgcctggga 360

aatgaccatc cagtaccgta atgcgggtat gttaacgcgg tcacagggta caccagaatc 420

cggatcgtct aacccccctta gcgggattcg ctaaaagatc accgagttag tgtgcaagaa 480

taatgctgat cgcaggggca ctgtcatacg ctgtcatgca gtcaatgaac agtgcggtgc 540

tctgtcgtga agaaaatcaa aaccaggagg gtttta gtg tca gtc gag acc agg 594

Val Ser Val Glu Thr Arg

1 5

aag atc acc aag gta ctt gtc gcc aac cgt ggt gaa atc gca atc cgt 642

Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile Arg

10 15 20

gtt ttc cgc gca gca cgg gat gaa ggc atc gcc tct gtc gcc gtc tac 690

Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr

25 30 35

gcg gag ccg gac gca gat gcc cct ttc gtc gag tat gcc gat gag gcc 738

Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Glu Tyr Ala Asp Glu Ala

40 45 50

ttc gca ctc ggt ggc cag act tcc gca gag tcc tac ctc gtc att gac 786

Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp

55 60 65 70

aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc 834

Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pr

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                    75                  80                  85
ggc tac ggc ttc ctc gcc gag aac gcc gat ttc gct gaa gct gtc atc   882
Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
                90                  95                  100
aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc   930
Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
        105                 110                 115
ctc ggt gac aag gtc acc gca cgc cac atc gcc aac aac gcc aac gca   978
Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
    120                 125                 130
ccg atg gca ccg ggc acc aag gag cct gtc aag gac gcc gct gag gtt  1026
Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu Val
135                 140                 145                 150
gtc gcc ttc gcc gag gag ttc ggt ctc ccc atc gcc atc aag gct gcc  1074
Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala Ala
                155                 160                 165
ttc ggt ggc ggc gga cgt ggc atg aag gtc gcc tac gag atg gac gaa  1122
Phe Gly Gly Gly Gly Arg Gly Met Lys Val Ala Tyr Glu Met Asp Glu
            170                 175                 180
gtc gcc gac ctc ttc gaa tcc gcc acc cgt gag gcc acc gcc gcc ttc  1170
Val Ala Asp Leu Phe Glu Ser Ala Thr Arg Glu Ala Thr Ala Ala Phe
        185                 190                 195
ggt cgt ggt gag tgc ttc gtg gag cgc tac ctg gac aag gcc cgc cac  1218
Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr Leu Asp Lys Ala Arg His
    200                 205                 210
gtc gag gca cag gtc atc gcc gac aag cac ggc aac gtt gtg gtc gcc  1266
Val Glu Ala Gln Val Ile Ala Asp Lys His Gly Asn Val Val Val Ala
215                 220                 225                 230
ggt acc cgt gac tgc tcc ctg cag cgt cgt ttc cag aag ctc gtc gag  1314
```

Gly Thr Arg Asp Cys S r Leu Gln Arg Arg Phe Gln Lys Leu Val Glu
235 240 245

gag gca ccg gca ccg ttc ctc acc gat gag cag cgt gac cgc atc cac 1362
Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu Gln Arg Asp Arg Ile His
250 255 260

tcc tcc gcc aag gct atc tgc cgc gag gcc ggt tac tac ggt gcc ggc 1410
Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala Gly Tyr Tyr Gly Ala Gly
265 270 275

acc gtg gag tac ctg gtc ggt tcc gac gga ctg atc tcc ttc ctg gag 1458
Thr Val Glu Tyr Leu Val Gly Ser Asp Gly Leu Ile Ser Phe Leu Glu
280 285 290

gtc aac acc cgc ctg cag gtg gag cac ccc gtc acc gag gag acc acc 1506
Val Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr Thr
295 300 305 310

ggc atc gac ctg gtg cgc gag atg ttc cgc atc gcc gag ggc gcc gag 1554
Gly Ile Asp Leu Val Arg Glu Met Phe Arg Ile Ala Glu Gly Ala Glu
315 320 325

ctc tcc atc aag gag gac ccg acc cca cgc ggc cac gcc ttc gag ttc 1602
Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg Gly His Ala Phe Glu Phe
330 335 340

cgc atc aac ggc gag gac gca ggc tcc aac ttc atg ccc gca ccg ggc 1650
Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn Phe Met Pro Ala Pro Gly
345 350 355

aag atc acc cgc tac cgt gag ccc gcc ggc ccg ggt gtc cgc atg gac 1698
Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly Pro Gly Val Arg Met Asp
360 365 370

tcc ggc gtt gtc gag ggt tcc gag atc tcc ggc cag ttc gac tcc atg 1746
Ser Gly Val Val Glu Gly Ser Glu Ile Ser Gly Gln Phe Asp Ser Met
375 380 385 390

```
ctg gcc aag ctg atc gtc tgg ggc cag acc cgt gag cag gcc ctg gag   1794
Leu Ala Lys Leu Ile Val Trp Gly Gln Thr Arg Glu Gln Ala Leu Glu
                395                 400                 405

cgt tcc cgt cgt gcg ctc ggc gag tac atc gtc gag ggc atg ccg acc   1842
Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile Val Glu Gly Met Pro Thr
            410                 415                 420

gtc atc ccg ttc cac tcc cac atc gtc tcc aac ccg gca ttc gtc ggt   1890
Val Ile Pro Phe His Ser His Ile Val Ser Asn Pro Ala Phe Val Gly
        425                 430                 435

gac ggc gag ggc ttc gag gtc tac acc aag tgg atc gag gag gtc tgg   1938
Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys Trp Ile Glu Glu Val Trp
    440                 445                 450

gac aac ccg atc gag ccg ttc gtc gat gca gcc gac ctc gac gac gac   1986
Asp Asn Pro Ile Glu Pro Phe Val Asp Ala Ala Asp Leu Asp Asp Asp
455                 460                 465                 470

gag gag aag acc ccg tcg cag aag gtc atc gtc gag atc gac ggc cgc   2034
Glu Glu Lys Thr Pro Ser Gln Lys Val Ile Val Glu Ile Asp Gly Arg
                475                 480                 485

cgc gtc gag gtg gct ctc ccg ggc gac ctc gct ctc ggc ggt ggc gca   2082
Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Gly Ala
            490                 495                 500

ggt gcc gcc aag aag aag ccg aag aag cgt cgc gca ggt ggc gcc aag   2130
Gly Ala Ala Lys Lys Lys Pro Lys Lys Arg Arg Ala Gly Gly Ala Lys
        505                 510                 515

gcc ggt gtc tcc ggt gac tcc gtc gca gcc ccg atg cag ggc acc gtc   2178
Ala Gly Val Ser Gly Asp Ser Val Ala Ala Pro Met Gln Gly Thr Val
    520                 525                 530

atc aag gtc aac gtt gag gac ggc gcc gag gtc tcc gag ggt gac acc   2226
Ile Lys Val Asn Val Glu Asp Gly Ala Glu Val Ser Glu Gly Asp Thr
```

535 540 545 550

gtc gtg gtt ctc gag gcc atg aag atg gag aac ccg gtc aag gcc cac 2274
Val Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His
555 560 565

aag tcc ggt acc gtc tcc ggt ctg acc atc gcc gcg ggt gag ggc gtg 2322
Lys Ser Gly Thr Val Ser Gly Leu Thr Ile Ala Ala Gly Glu Gly Val
570 575 580

acc aag ggt cag gtt ctc ctg gag atc aag taatcccttc agggaacaga 2372
Thr Lys Gly Gln Val Leu Leu Glu Ile Lys
585 590

cagccctgtt ct 2384

【００７０】

<210> 4

<211> 592

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 4

Val Ser Val Glu Thr Arg Lys Ile Thr Lys Val Leu Val Ala Asn Arg
1 5 10 15

Gly Glu Ile Ala Ile Arg Val Phe Arg Ala Ala Arg Asp Glu Gly Ile
20 25 30

Ala Ser Val Ala Val Tyr Ala Glu Pro Asp Ala Asp Ala Pro Phe Val
35 40 45

Glu Tyr Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu
50 55 60

Ser Tyr Leu Val Ile Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly
65 70 75 80

Ala Asp Ala Val His Pr Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp

85 90 95

Phe Ala Glu Ala Val Ile Asn Glu Gly Leu Ile Trp Ile Gly Pr Ser

100 105 110

Pro Glu Ser Ile Arg Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile

115 120 125

Ala Asn Asn Ala Asn Ala Pro Met Ala Pro Gly Thr Lys Glu Pro Val

130 135 140

Lys Asp Ala Ala Glu Val Val Ala Phe Ala Glu Glu Phe Gly Leu Pro

145 150 155 160

Ile Ala Ile Lys Ala Ala Phe Gly Gly Gly Gly Arg Gly Met Lys Val

165 170 175

Ala Tyr Glu Met Asp Glu Val Ala Asp Leu Phe Glu Ser Ala Thr Arg

180 185 190

Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr

195 200 205

Leu Asp Lys Ala Arg His Val Glu Ala Gln Val Ile Ala Asp Lys His

210 215 220

Gly Asn Val Val Val Ala Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg

225 230 235 240

Phe Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu

245 250 255

Gln Arg Asp Arg Ile His Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala

260 265 270

Gly Tyr Tyr Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly

275 280 285

Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln Val Glu His Pro

290 295 300

Val Thr Glu Glu Thr Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg

305 310 315 320

Ile Ala Glu Gly Ala Glu Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg
325 330 335
Gly His Ala Phe Glu Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn
340 345 350
Phe Met Pro Ala Pro Gly Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly
355 360 365
Pro Gly Val Arg Met Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser
370 375 380
Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val Trp Gly Gln Thr
385 390 395 400
Arg Glu Gln Ala Leu Glu Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile
405 410 415
Val Glu Gly Met Pro Thr Val Ile Pro Phe His Ser His Ile Val Ser
420 425 430
Asn Pro Ala Phe Val Gly Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys
435 440 445
Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Glu Pro Phe Val Asp Ala
450 455 460
Ala Asp Leu Asp Asp Asp Glu Glu Lys Thr Pro Ser Gln Lys Val Ile
465 470 475 480
Val Glu Ile Asp Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu
485 490 495
Ala Leu Gly Gly Gly Ala Gly Ala Ala Lys Lys Lys Pro Lys Lys Arg
500 505 510
Arg Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ser Val Ala Ala
515 520 525
Pro Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Asp Gly Ala Glu
530 535 540
Val Ser Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu

545 550 555 560

Asn Pro Val Lys Ala His Lys Ser Gly Thr Val Ser Gly Leu Thr Ile

565 570 575

Ala Ala Gly Glu Gly Val Thr Lys Gly Gln Val Leu Leu Glu Ile Lys

580 585 590

【００７１】

<210> 5

<211> 2128

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (339)..(1967)

<400> 5

gctgtcattc cgaccacatt cgccccggga tccgggctcc accacctccc ggacccatgc 60

cccatacctg cggaaaccac gggaaacacg ggaaaaaccg atctcattca gaccggcggg 120

atccacctgt ggaacagtca gcggcgcggc catggagggc agcgacaggt gacgtccgag 180

cacccggttc cccaccgtgg acacggcatt gatccgacac ggtggggata gtttcatgct 240

gaaaaactat cgctgtgcag ggaggatccg gaatgtgacc tatttcatgg agaaatgatt 300

gtggacgata cccccgggta cggctaccat tccaaaac atg acc att tcc tca cct 356

Met Thr Ile Ser Ser Pro

1 5

ttg att gac gtc gct aac ctg cca gac atc aac acc acc gcc ggc aag 404

Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys

10 15 20

atc gcc gac ctg aag gcc cgc cgg gcg gaa gcc cac ttc ccc atg ggt 452

Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pr Met Gly

```
          25                  30                  35
gaa aag gcc gta gag aag gtc cac gcg gcc aac cgc ctc acc gcg cgc   500
Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg
     40                  45                  50
gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc gat   548
Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp
 55                  60                  65                  70
cag ctc gca cgc cac cgc acc acc gcg ttc ggc ctg ggc aac aag cga   596
Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg
                 75                  80                  85
ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc   644
Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg
             90                  95                 100
gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc   692
Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala Leu
        105                 110                 115
ggt gag gtc tac ggc gag aag atg atc aag atc atg gag ctg gcc atc   740
Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala Ile
    120                 125                 130
gac acc ggc cgc cca ctc atc ggc ctg tac gag ggt gca ggt gcc cgc   788
Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala Arg
135                 140                 145                 150
atc cag gac ggt gcg gtc tcc ctc gac ttc atc tcc cag acc ttc tat   836
Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe Tyr
                155                 160                 165
cag aac atc cag gcc tcc ggc gtg atc ccg cag atc tcc gtg atc atg   884
Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile Met
            170                 175                 180
ggt gcc tgc gcc ggt ggc aac gcc tac ggc ccg gcc ctg acc gac ttc   932
```

```
Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp Phe
        185                 190                 195
gtg gtc atg gtg gac aag acc tcg aag atg ttc gtc acc ggc ccc gat   980
Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro Asp
    200                 205                 210
gtg atc aag acc gtc acc ggc gag gag atc acc cag gag gag ctc ggc   1028
Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu Gly
215                 220                 225                 230
gga gca acc acc cac atg gtc acc gcc ggc aac tcc cac tac acc gtc   1076
Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr Val
                235                 240                 245
gcc acc gat gag gag gcc ctc gac tgg gtc cag gac ctc atc tcc ttc   1124
Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Ile Ser Phe
            250                 255                 260
ctg ccc tcc aac aat cgc tcc tac gcc ccg gtg gag gag ttc gac gag   1172
Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Val Glu Glu Phe Asp Glu
        265                 270                 275
gag gac ggt ggc atc gcc gag aac atc acc gcc gat gac ctg aag ctg   1220
Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr Ala Asp Asp Leu Lys Leu
    280                 285                 290
gat gag atc atc ccg gat tcc gcc acc gtg ccc tat gat gtc cgc gac   1268
Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg Asp
295                 300                 305                 310
gtc atc cag tgc ctg acc gac gac ggt gag tac ctg gag atc cag gcc   1316
Val Ile Gln Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln Ala
                315                 320                 325
gac cga gcc gag aat gtc gtc atc gcc ttc ggc cgc atc gag ggc cag   1364
Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly Gln
            330                 335                 340
```

tcc gtc ggt ttc gtc gcc aac cag ccg acc cag ttc gcc ggc tgc ctg 1412
Ser Val Gly Ph Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu
345 350 355

gac atc gac tcc tcc gag aag gca gcc cgc ttc gtc cgc acc tgc gat 1460
Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys Asp
360 365 370

gcc ttc aac atc ccg atc gtc atg ctt gtc gac gtc ccc ggc ttc ctc 1508
Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe Leu
375 380 385 390

ccc ggt gcc ggc cag gag tac ggc ggc atc ctg cgt cgt ggc gcc aaa 1556
Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys
395 400 405

ctg ctc tac gcc tac ggt gag gcc acc gtc ccg aag atc acc gtg acc 1604
Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val Thr
410 415 420

atg cgc aag gcc tac ggc ggt gcg tac tgt gtc atg gga tcc aag ggt 1652
Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly
425 430 435

ctg ggc gca gac atc aac ctg gcc tgg ccg acc gcg cag atc gcc gtc 1700
Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val
440 445 450

atg ggt gcc gcc ggc gcg gtc cag ttc atc tac cgc aag gag ctc atg 1748
Met Gly Ala Ala Gly Ala Val Gln Phe Ile Tyr Arg Lys Glu Leu Met
455 460 465 470

gcc gct gat gcc aag ggc ctg gac acc gtc gcc ctg gcc cag tcc ttc 1796
Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Gln Ser Phe
475 480 485

gag cgt gag tac gag gac cac atg ctc aac ccg tac ctg gcg gcc gag 1844
Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr Leu Ala Ala Glu

490 495 500

cgt ggc ctc atc gac gcg gtg atc ctg ccg tcc gag acc cgt ggc cag 1892
Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln

505 510 515

atc gca cgc aac ctg cgt ctg ctc aag cac aag aat gtc tcc cgc cct 1940
Ile Ala Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Ser Arg Pro

520 525 530

gcc cgc aag cac ggc aac atg cca ctg taagcacccg ggaccacccc 1987
Ala Arg Lys His Gly Asn Met Pro Leu

535 540

ctacgcccgc acccacggcc ctttgctggc aggtgcgggc gctgtgcgtt ttccgcgcct 2047
gccgacgccc ggccccctgc cctgtgatgc gatctgcgga tgtgatctgc gcccgcgcca 2107
actcccctgg ttgaaccctg c 2128

【００７２】

<210> 6

<211> 543

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 6

Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
1 5 10 15

Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
20 25 30

Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
35 40 45

Asn Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
50 55 60

Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe

65 70 75 80

Gly Leu Gly Asn Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp

85 90 95

Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr

100 105 110

Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys

115 120 125

Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr

130 135 140

Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe

145 150 155 160

Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro

165 170 175

Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly

180 185 190

Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met

195 200 205

Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile

210 215 220

Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly

225 230 235 240

Asn Ser His Tyr Thr Val Ala Thr Asp Glu Glu Ala Leu Asp Trp Val

245 250 255

Gln Asp Leu Ile Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro

260 265 270

Val Glu Glu Phe Asp Glu Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr

275 280 285

Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val

290 295 300

Pro Tyr Asp Val Arg Asp Val Ile Gln Cys Leu Thr Asp Asp Gly Glu
305 310 315 320
Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
325 330 335
Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
340 345 350
Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
355 360 365
Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
370 375 380
Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile
385 390 395 400
Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val
405 410 415
Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys
420 425 430
Val Met Gly Ser Lys Gly Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro
435 440 445
Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gln Phe Ile
450 455 460
Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
465 470 475 480
Ala Leu Ala Gln Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
485 490 495
Pro Tyr Leu Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro
500 505 510
Ser Glu Thr Arg Gly Gln Ile Ala Arg Asn Leu Arg Leu Leu Lys His
515 520 525
Lys Asn Val Ser Arg Pro Ala Arg Lys His Gly Asn Met Pr Leu

530 535 540

【００７３】

<210> 7

<211> 2076

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (412)..(2022)

<400> 7

acgcccggcc ccctgccctg tgatgcgatc tgcggatgtg atctgcgccc gcgccaactc 60

ccctggttga accctgccac ataccctgag tcgcacctgg gtggggtcac tttccacctc 120

acgggggggа ggaggtcaca taggccatac gctgcacttt tgatgaagtg tgggcagatc 180

gaccgggcaa atctgggaaa taaggggcct ggtgaactag cattcccctt agcgaagggt 240

gagcatcgcg gaccccgcga tgtcccaacc ggtcgtaaat tcatgtgccg ccacagtccc 300

ctcaccaggg gatcggaacc agcccagcct gattccggcg tgacggacct caccgtgaac 360

aagtccccgc attactcaca gaactcacac caggatttag actaagaaac c atg act 417

Met Thr

1

gca gca acg aca gca cct gat ctg acc acc acc gcc ggc aaa ctc gcg 465

Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ala

5 10 15

gat ctc cgc gcc cgc ctt tcc gag acc cag gcc ccc atg ggt cag gcc 513

Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly Gln Ala

20 25 30

tcc gtg gag aag gtg cac gag gca ggg aag aag acc gca cgc gag cgc 561

Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg Glu Arg

35 40 45 50

atc gag tac ctg ctc gat gag ggc tcc ttc gtt gag gtc gat gcc ctc 609
Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp Ala Leu
55 60 65

gcc cgc cac cgt tcc aag aac ttc ggc ctg gac tcc aag cgc ccg gtc 657
Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val
70 75 80

acc gac ggt gtg gtc acc ggt tac ggc acc atc gac gga cgc aag gtc 705
Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val
85 90 95

tgc gtc ttc tcc cag gac ggc gct atc ttc ggc ggt gcc ctc ggt gag 753
Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu
100 105 110

gtc tac ggc gag aag atc gtc aag atc atg gac ctg gcc atc aag acc 801
Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr
115 120 125 130

ggt gtc ccc ctc atc ggc atc aac gag ggc gcc ggc gcc cgc atc cag 849
Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln
135 140 145

gaa ggc gtt gtc tcc ctg ggc ctg tac tcc cag atc ttc tac cgc aac 897
Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn
150 155 160

acc cag gca tcc ggt gtc atc cca cag atc tcc ctc atc atg ggt gcc 945
Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala
165 170 175

tgc gcc ggt ggc cat gtg tac tcc ccc gcc ctg acc gac ttc atc atc 993
Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Ile
180 185 190

atg gtg gac aag acc tcc aag atg ttc atc acc ggc ccc gac gtg atc 1041

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Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp Val Ile
195                 200                 205                 210
aag acc gtc acc ggc gag gag gtc acc cag gag gaa ctg ggt ggt gcc   1089
Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly Gly Ala
                215                 220                 225
tac acc cac atg gcc cag tcc ggc acc tcg cac tac acc gca gcc gat   1137
Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala Ala Asp
            230                 235                 240
gac tcc gat gcc ctc gac tgg gtc cgt gag ctg gtc agc tac ctg ccg   1185
Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr Leu Pro
        245                 250                 255
tcc aac aac cgt gcg gag acc cca cgc cag gac gcc gac atc atg gtg   1233
Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile Met Val
    260                 265                 270
ggc tcc atc aag gag aac atc acc gag acc gac ctc gaa ctc gac acc   1281
Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu Asp Thr
275                 280                 285                 290
ctg atc ccg gat tcc ccg aac cag ccg tac gac atg aag gac gtc atc   1329
Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp Val Ile
                295                 300                 305
acc cgc atc gtc gat gat gcc gag ttc ttc gag atc cag gag ggt tac   1377
Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Gly Tyr
            310                 315                 320
gcc gag aac atc atc tgc ggt ttc gcc cgc gtc gag ggt cgt gcc gtg   1425
Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg Ala Val
        325                 330                 335
ggt atc gtg gcc aac cag ccg atg cag ttc gcc ggc tgc ctg gac atc   1473
Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu Asp Ile
    340                 345                 350
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aag gca tcc gag aag gcc gcc cgc ttc atc cgc acc tgt gac gcc ttc 1521
Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe
355 360 365 370
aac atc ccg atc atc gag ctt gtc gac gtc cca ggc ttc ctc ccg ggc 1569
Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu Pro Gly
375 380 385
acc aac cag gag ttc gac ggc atc atc cgt cgc ggc gcg aag ctg ctc 1617
Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu
390 395 400
tac gcc tac gcc gag gcc acc gtc ggc aag atc acc gtg atc acc cgc 1665
Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg
405 410 415
aag tcc tac ggc ggt gcc tac tgc gtg atg ggc tcc aag gac atg ggt 1713
Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly
420 425 430
gcg gac ctc gtc ttc gca tgg ccc acc gcg cag atc gcc gtc atg ggt 1761
Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly
435 440 445 450
gcc tcc ggt gcc gtc ggc ttc atc tac cgc aag gag ctc aag cag gct 1809
Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys Gln Ala
455 460 465
gca gcg gcc ggc gag gat gtc acc gcg ctg atg aag aag tac gag cag 1857
Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr Glu Gln
470 475 480
gag tac gag gag acc ctg gtc aac ccg tac atg gct gca gag cgt ggc 1905
Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu Arg Gly
485 490 495
tac gtc gac gcc gtc atc cca cca tcc gag acc cgt ggt cag atc atc 1953
Tyr Val Asp Ala Val Ile Pr Pr Ser Glu Thr Arg Gly Gln Ile Ile

500 505 510

gag ggt ctg cgt ctg ctc gac cgc aag gtg gtc aac gtc ccg gcc aag 2001
Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro Ala Lys
515 520 525 530

aag cac ggt aac atc ccg ctg taaaccgtct tcccctccgg caccacgccg 2052
Lys His Gly Asn Ile Pro Leu
535

gagaaggctt tgtccgcagc tgtc 2076

［００７４］

<210> 8

<211> 537

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 8

Met Thr Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys
1 5 10 15

Leu Ala Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly
20 25 30

Gln Ala Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg
35 40 45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp
50 55 60

Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg
65 70 75 80

Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
85 90 95

Lys Val Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu
100 105 110

Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile
115 120 125
Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
130 135 140
Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
145 150 155 160
Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
165 170 175
Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
180 185 190
Ile Ile Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp
195 200 205
Val Ile Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly
210 215 220
Gly Ala Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala
225 230 235 240
Ala Asp Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr
245 250 255
Leu Pro Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile
260 265 270
Met Val Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu
275 280 285
Asp Thr Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp
290 295 300
Val Ile Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu
305 310 315 320
Gly Tyr Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg
325 330 335
Ala Val Gly Ile Val Ala Asn Gln Pr Met Gln Phe Ala Gly Cys Leu

340 345 350

Asp Ile Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp

355 360 365

Ala Phe Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu

370 375 380

Pro Gly Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys

385 390 395 400

Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile

405 410 415

Thr Arg Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp

420 425 430

Met Gly Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val

435 440 445

Met Gly Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys

450 455 460

Gln Ala Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr

465 470 475 480

Glu Gln Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu

485 490 495

Arg Gly Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln

500 505 510

Ile Ile Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro

515 520 525

Ala Lys Lys His Gly Asn Ile Pro Leu

530 535

【００７５】

<210> 9

<211> 1643

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (326)..(1363)

<400> 9

agcgcgccgg cagccaccag tgggatcgtg cccagcggac ggatgccgga ttcacggcgg 60

tcagccaccc gccgatgaga cctgcagcga caacggtggc ggtgctgacc tggtcagcgt 120

ctttgagttt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180

ctggggtggc ggacaccatg tccgttcggg cgttgccccg acgggggaaa atcgcaggca 240

gatgtgtccg atgtgggata aacccaccgg ttcgggcgtg tcttcgggat caatggcaca 300

gcattaaccg tgtgggggt ttaat atg gga gcc atg cga att gcc act ctc 352

Met Gly Ala Met Arg Ile Ala Thr Leu

1 5

acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc 400

Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile

10 15 20 25

gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag 448

Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln

30 35 40

gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac 496

Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp

45 50 55

gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc 544

Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly

60 65 70

acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc 592

Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val

75 80 85

aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt 640
Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly
90 95 100 105

ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc 688
Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile
110 115 120

ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg 736
Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr
125 130 135

gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc 784
Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala
140 145 150

atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc 832
Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile
155 160 165

gtc gag gtc atg ggc cgc cac gtc ggt tgg atc gca ctg cat gcc ggc 880
Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly
170 175 180 185

atg gcc ggt gga gcc cac tac acc gtc atc ccc gag gtg ccc ttc gac 928
Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp
190 195 200

atc tcg gag atc tgc aag cgt atg gaa cgt cgc ttc cag atg ggg gag 976
Ile Ser Glu Ile Cys Lys Arg Met Glu Arg Arg Phe Gln Met Gly Glu
205 210 215

aag tac ggc atc atc gtc gtc gcg gag ggt gcc ctg ccc aag gag gga 1024
Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Lys Glu Gly
220 225 230

acc atg gag ctg cgt gag ggg gag gtg gat cag ttc ggt cac aag acc 1072

Thr Met Glu Leu Arg Glu Gly Glu Val Asp Gln Phe Gly His Lys Thr
235 240 245

ttc acc ggc atc ggc cag cag atc gcc gac gag gtg cac agg cgt ctg 1120
Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Val His Arg Arg Leu
250 255 260 265

ggt cat gat gtc cgc acc acg gtc ctg ggc cat atc cag cgt ggt ggc 1168
Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly
270 275 280

acc ccc acc gcc ttc gac cgt gtc ctg gcc acc cgg tac ggt gtc cgc 1216
Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg
285 290 295

gcc gcg cgt gcc tgc cac gag ggt cag ttc aac acc gtg gtc gcg ctc 1264
Ala Ala Arg Ala Cys His Glu Gly Gln Phe Asn Thr Val Val Ala Leu
300 305 310

aag ggg gag cgc atc cgg atg atc tcc ttc gat gag gcc gtg ggc acc 1312
Lys Gly Glu Arg Ile Arg Met Ile Ser Phe Asp Glu Ala Val Gly Thr
315 320 325

ctg aag aag gtg ccg atg gaa cgc tgg gtg acc gcc cag gct atg ttc 1360
Leu Lys Lys Val Pro Met Glu Arg Trp Val Thr Ala Gln Ala Met Phe
330 335 340 345

ggt tagtcaggcc gcattcccgg ttccgcgccc gcggggccgg gttttttcat 1413
Gly

gccccggaac acatcggtat gaaatcgtga tatgcattac ttgacgggga agtgggggat 1473

ccgtcacctc gcgttgtcca actacagccc gcagcgcctg cgggaattct tcgagcaatc 1533

cgccgattcc ccggcccgtc ccgtcgccgt ccaaccgcag tacaatctgc tggcccgccg 1593

ggattatgag accggtatcc gcccggtcgt ggacgagttc ggtcccgcgg 1643

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<210> 10

<211> 346

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 10

Met Gly Ala Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
1 5 10 15

Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
20 25 30

Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
35 40 45

Ala Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
50 55 60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
65 70 75 80

Lys Phe Arg Ala Gly Ile Asp Gln Val Lys Ala Asn Leu Ala Asp Ala
85 90 95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
100 105 110

Ala Lys Trp Leu Ala Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
115 120 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
130 135 140

Ser Ala Val Ser Val Ala Thr Asp Ala Ile Asp Arg Leu His Thr Thr
145 150 155 160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
165 170 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
180 185 190

Thr Val Ile Pr Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Arg

195 200 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val

210 215 220

Ala Glu Gly Ala Leu Pro Lys Glu Gly Thr Met Glu Leu Arg Glu Gly

225 230 235 240

Glu Val Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln

245 250 255

Ile Ala Asp Glu Val His Arg Arg Leu Gly His Asp Val Arg Thr Thr

260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg

275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu

290 295 300

Gly Gln Phe Asn Thr Val Val Ala Leu Lys Gly Glu Arg Ile Arg Met

305 310 315 320

Ile Ser Phe Asp Glu Ala Val Gly Thr Leu Lys Lys Val Pro Met Glu

325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly

340 345

【００７７】

<210> 11

<211> 498

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(498)

<400> 11

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tac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggt   48
Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1               5                  10                  15

tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg   96
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
            20                  25                  30

acg cac ctg ccc gat gct ctt tac ccg gat gta tcc tat gac ctg gat  144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
        35                  40                  45

gga tgc tat tcc ggc gga gcc gta ttt tct gac ggc acg ctt aaa ctt  192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
    50                  55                  60

ttc tac acc ggc aac cga aaa att gac ggc aag cgc cgc gcc acc caa  240
Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65                  70                  75                  80

aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat  288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
                85                  90                  95

cgc cgc tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttt  336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
            100                 105                 110

acg ccc cac tac cgc gat ccc atg atc agc cct gat ggg gat ggt tgg  384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
        115                 120                 125

aag atg gtt ctt ggg gct cag cgc gaa aac ctc acc ggt gca gcg gtt  432
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
    130                 135                 140

cta tac cgc tcg gca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc  480
```

Leu Tyr Arg S r Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
145 150 155 160

acc ttt gac ctc agc gac 498
Thr Phe Asp Leu Ser Asp
165

【0078】

<210> 12

<211> 166

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 12

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15

Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30

Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
35 40 45

Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
50 55 60

Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65 70 75 80

Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95

Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110

Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125

Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val

130 135 140

Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
145 150 155 160

Thr Phe Asp Leu Ser Asp
165

【００７９】

<210> 13

<211> 479

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<400> 13

tac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc 48
Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15

tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30

acg cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat 144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
35 40 45

gga tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt 192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
50 55 60

ttc tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa 240

Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65 70 75 80

aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95

cgc cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc 336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110

aca ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggc tgg 384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125

aaa atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt 432
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
130 135 140

cta tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa at 479
Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
145 150 155

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<210> 14

<211> 159

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 14

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15

Trp Ala His Thr Thr Thr Pr Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30

Thr His Leu Pro Asp Ala Leu Tyr Pr Asp Ala Ser Tyr Asp Leu Asp

35 40 45

Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu

50 55 60

Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln

65 70 75 80

Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His

85 90 95

Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe

100 105 110

Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp

115 120 125

Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val

130 135 140

Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu

145 150 155

【００８１】

<210> 15

<211> 490

<212> DNA

<213> Corynebacterium thermoaminogenes

<400> 15

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tttagaacct ggagatgaag aagaaaaatg gttgtttctc tggtacaggt atagtcaaag 180

atgataagtt gtatttattt tatacaggtc accattatta taatgacgat gatcccgatc 240

atttttggca aaatcaaaat atggcttata gtgaagatgg cattcatttt caaaaatata 300

aacaaaatgc aatcattcct accccacctg aagataatac acatcacttc agagatccaa 360

aggtatggga acatccatgg cttattatta catgatagta ggtagtcaaa atgatagaga 420

attaggacgt attatcttat atcgttctga ggatttatag aggggaattc tggtcctgag 480

490

atcaatccaa

【００８２】

<210> 16

<211> 4254

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (637)..(1362)

<220>

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<222> (1434)..(2315)

<220>

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<222> (2432)..(3115)

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<222> (3235)..(4065)

<400> 16

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cgcaggtgtt gaagacgatg agatcagggg tgtcaccctc ccccgccgcg gtgtaaccgg 120

cctcctcgag cagaccggag agacgctcgg aatcgtggac gttcatctgg cagccgaagg 180

tacgcacctc ataggtgcgg gcagtggtgc cctcccggtt cccccgcgcc gggagggtgt 240

cggcggggtg gtccgggtgg gatggatggg tgttcatctg gtgggtatca atctgctgcg 300

tcacgggagg taattgtatc ggccgcgggc accctgacat aaacgtccga tccagaggaa 360

cgcaaccccg tggagtgtcg cagccatgca ggttgggcaa caccgtaacg gaacctagca 420

gagtggtagg attgacttca cattctttac ctattgagct attgataaaa tccgggcgga 480

aatggaaatc acccccacaa atcaccccaa ctgacctgtg gaaagggcga gaaatccagg 540

gaaattcatt tcaaaatgga ctcaatcaca ggatttaccc cacatgaccc aacattcctt 600

tatgctatcc ccatgacgca gaccacaaat cacccg atg atc aag atg acg ggg 654
Met Ile Lys Met Thr Gly
1 5

gtg cag aag ttc ttc gat gac ttc cag gcc ctg acc gat atc aat ctt 702
Val Gln Lys Phe Phe Asp Asp Phe Gln Ala Leu Thr Asp Ile Asn Leu
10 15 20

gag gtc ccc gcg gga cag gtc gtt gtt gtt ctc ggc ccg tcc ggt tcc 750
Glu Val Pro Ala Gly Gln Val Val Val Val Leu Gly Pro Ser Gly Ser
25 30 35

gga aag tcg acg ctg tgc cgc acc atc aac cgc ctc gaa acc atc gag 798
Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg Leu Glu Thr Ile Glu
40 45 50

gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag 846
Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys
55 60 65 70

gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc 894
Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe
75 80 85

aac ctc ttc ccc cac ctc acc atc aag gac aat gtc acc ctc ggc ccg 942
Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro
90 95 100

atg aag gtc cgg aag atg aag aag tcc gag gcc aat gag gtg gcc atg 990
Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met
105 110 115

aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg 1038

Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro
120 125 130

gca cag ctc tcg ggc ggg cag cag cag cgc gtg gcc atc gcc cgc gca 1086
Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala
135 140 145 150

ctg gcg atg aac ccc aag atc atg ctt ttc gac gaa cca acc tcc gcc 1134
Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp Glu Pro Thr Ser Ala
155 160 165

ctc gac ccc gag atg gtc aac gag gtt ctg gac gtc atg gcg agt ctg 1182
Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp Val Met Ala Ser Leu
170 175 180

gcc aag gaa ggc atg acc atg gtg tgt gtc acc cac gag atg ggt ttc 1230
Ala Lys Glu Gly Met Thr Met Val Cys Val Thr His Glu Met Gly Phe
185 190 195

gca cgc agg gcc gca gac cgt gtg ctg ttc atg tct gac ggc gcc atc 1278
Ala Arg Arg Ala Ala Asp Arg Val Leu Phe Met Ser Asp Gly Ala Ile
200 205 210

gtc gag gac tcc gac ccg gag acc ttc ttc acc aat cca caa acc gac 1326
Val Glu Asp Ser Asp Pro Glu Thr Phe Phe Thr Asn Pro Gln Thr Asp
215 220 225 230

cgg gcg aag gat ttc ctg ggc aag atc ctc gcc cac tgacctcccc 1372
Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala His
235 240

tcactctgtg tccaactccc ccgctggcca aaatcagcga ccatgaccaa caggagcatc 1432

a atg tcg cac aaa cgc atg ttc acc cgt ctc gcc gca gcc acc agc gca 1481
Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala
245 250 255

gct gtt ctc gcc ggc atc acc ctc acc gcc tgt ggt gat tcc gag ggt 1529
Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly

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    260                 265                 270
ggt gac ggt ctg ctc gcc gcc atc gaa aat ggc aat gtc acc atc ggc   1577
Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
275                 280                 285                 290
acc aag tac gat cag ccg ggt ctg gga ctg cgt aac ccg gac aat tcc   1625
Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
                295                 300                 305
atg agc gga ctg gat gtc gac gtc gcg cag tac gtg gtc aac tcc atc   1673
Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
            310                 315                 320
gcc gat gac aac ggt tgg gat cac ccc acc gtg gaa tgg cgc gag acc   1721
Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
        325                 330                 335
ccc tcc gcc cag cgc gag acc ctc atc cag aac ggt gag gtg gat atg   1769
Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
    340                 345                 350
atc gcc gca acc tac tcc atc aac ccc gga cgc tcc gaa tcg gtg aac   1817
Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
355                 360                 365                 370
ttc ggt gga cca tac ctc ctc acc cac cag gcc ctc ctg gtc cgc gag   1865
Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
                375                 380                 385
gac gat gac cgc atc cag acc ctc gag gac ctc gat gac ggc ctg atc   1913
Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
            390                 395                 400
ctg tgt tcc gtt acc gga tcc acc ccc gcc cag aag gtc aag gat gtc   1961
Leu Cys Ser Val Thr Gly Ser Thr Pr  Ala Gln Lys Val Lys Asp Val
        405                 410                 415
ctc ccc ggc gtc cag ctg cag gaa tac gac acc tac tcc tcc tgt gtg   2009
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Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
    420                 425                 430
gag gca ctg agc cag ggc aac gtc gat gca atg acc acc gac gcc acc   2057
Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
435                 440                 445                 450
atc ctc ttc ggc tac gcg cag cag cgc gaa ggt gaa ttc cgc gtc gtg   2105
Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val
                455                 460                 465
gag atg gaa cag gac ggc gag ccg ttc acc aat gag tac tac ggc atc   2153
Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile
            470                 475                 480
ggt atc acc aag gat gac acc gaa gcc acc gat gcg atc aac gca gcg   2201
Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
        485                 490                 495
ttg gag cgt atg tac gcc gac ggt tcc ttc cag cgt ttc ctc acc gag   2249
Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
    500                 505                 510
aac ctc ggc gag gat tcc cag gtt gtc cag gag ggc acc ccg ggt gac   2297
Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
515                 520                 525                 530
ctc tcc ttc ctg gac gag tgacctgacg gggccgaacg cccgatgagc          2345
Leu Ser Phe Leu Asp Glu
                535
atgcgtggcc cccgcatccc ggggtgccac gcatcatcac tttcaccact gatcccctac 2405
cgttccttac cgaggagaaa ttcccc atg agt aca tta tgg gcg gat ctg ggt   2458
                              Met Ser Thr Leu Trp Ala Asp Leu Gly
                                    540                 545
ccg tca ctc cta ccc gca ttc tgg gtg aca atc caa ctc acc gtc tat   2506
Pro Ser Leu Leu Pr  Ala Phe Trp Val Thr Ile Gln Leu Thr Val Tyr
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                    550                 555                 560
tcc gcc atc gga tcc atg atc ctc ggt acc atc ctc acc gcc atg agg   2554
Ser Ala Ile Gly Ser Met Ile Leu Gly Thr Ile Leu Thr Ala Met Arg
                565                 570                 575
gtg tcc ccg gtg aag atc ctg cgc agc ata tcc acc gcc tac atc aac   2602
Val Ser Pro Val Lys Ile Leu Arg Ser Ile Ser Thr Ala Tyr Ile Asn
        580                 585                 590
acg gtc cgt aac acc cca ctg acc ctg gtg atc ctg ttc tgt tcc ttc   2650
Thr Val Arg Asn Thr Pro Leu Thr Leu Val Ile Leu Phe Cys Ser Phe
    595                 600                 605
ggc ctg tat cag aat ctc ggt ctc acc ctc gcc ggt cgc gac agt tcc   2698
Gly Leu Tyr Gln Asn Leu Gly Leu Thr Leu Ala Gly Arg Asp Ser Ser
610                 615                 620                 625
acc ttt ctg gcc gat aac aac ttc cgg ctc gcg gtg ctc gga ttc atc   2746
Thr Phe Leu Ala Asp Asn Asn Phe Arg Leu Ala Val Leu Gly Phe Ile
                630                 635                 640
ctg tac acc tcc gcc ttc gtt gcg gaa tca ctc cgg tca ggc atc aac   2794
Leu Tyr Thr Ser Ala Phe Val Ala Glu Ser Leu Arg Ser Gly Ile Asn
            645                 650                 655
acc gtg cac ttc ggg cag gcg gag gcc gcc cgg tcg ctg gga ctc ggt   2842
Thr Val His Phe Gly Gln Ala Glu Ala Ala Arg Ser Leu Gly Leu Gly
        660                 665                 670
ttc agt gac atc ttc cgg tcc atc atc ttc ccc cag gcg gtg cgt gcc   2890
Phe Ser Asp Ile Phe Arg Ser Ile Ile Phe Pro Gln Ala Val Arg Ala
    675                 680                 685
gcc atc atc ccg ctg ggc aac acc ctc atc gcc ctg acc aag aac acc   2938
Ala Ile Ile Pr  Leu Gly Asn Thr Leu Ile Ala Leu Thr Lys Asn Thr
690                 695                 700                 705
acg atc gcg tcc gtg atc ggc gtc ggt gag gcc tcg ctg ctg atg aag   2986
```

Thr Ile Ala Ser Val Il Gly Val Gly Glu Ala Ser Leu Leu Met Lys
710 715 720

tcc acg att gaa aat cat gcc aac atg ctc ttc gtc gtg ttc gcc atc 3034
Ser Thr Ile Glu Asn His Ala Asn Met Leu Phe Val Val Phe Ala Ile
725 730 735

ttc gcc gtc ggc ttc atg atc ctc acc ctc ccc atg ggc ctg ggg ctt 3082
Phe Ala Val Gly Phe Met Ile Leu Thr Leu Pro Met Gly Leu Gly Leu
740 745 750

gga aaa ctc gct gag aaa atg gcg gtg aag aaa taatgtcctc ctccgtacgc 3135
Gly Lys Leu Ala Glu Lys Met Ala Val Lys Lys
755 760

gcaacagtcc tctacgacgc ccccggcccc cggggacgca ggtccaacac catcatcacc 3195
atcgccacca ccctggtggc agtggccgtc ctgttctgg gtg ggc agt gtt ctc 3249
Val Gly Ser Val Leu
765

cag gaa aac ggc cag ttg gac ggc gac aaa tgg acc ccg ttc ctc gat 3297
Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp Thr Pro Phe Leu Asp
770 775 780 785

ccc cag acc tgg acc acc tat ctt ctg ccc ggc ctg tgg gga acc ctg 3345
Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly Leu Trp Gly Thr Leu
790 795 800

aag gca gcg gtg gcc tcc atc ctt ctc gcg ctg atc atg ggc acc ctg 3393
Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu Ile Met Gly Thr Leu
805 810 815

ctc ggg ctc gga cgc atc tcc gaa atc cgg ctc ctg cgc tgg ttc tgc 3441
Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu Leu Arg Trp Phe Cys
820 825 830

ggg atc atc atc gag acc ttc cgt gcc atc ccg gtg ctg atc ctc atg 3489
Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro Val Leu Ile Leu Met

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    835                 840                 845
atc ttc gcc tat cag ttg ttc gcc cgt tac cag ctc gtt cca tca cgc   3537
Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln Leu Val Pro Ser Arg
850                 855                 860                 865
cag ctg gcc ttc gcc gcg gtg gtc ttc ggt ctc acc atg tac aac ggc   3585
Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu Thr Met Tyr Asn Gly
                870                 875                 880
tcc gtc atc gcc gag atc ctt aga tcg ggt atc gcc tcc ctg ccg aag   3633
Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile Ala Ser Leu Pro Lys
            885                 890                 895
gga cag cgt gag gcg gcg atc gcc ctg ggc atg tca acc cgc cag acc   3681
Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met Ser Thr Arg Gln Thr
        900                 905                 910
acc tgg tcg atc ctg ctc ccc cag gcg gtg gca gcg atg ctg ccc gcc   3729
Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala Ala Met Leu Pro Ala
    915                 920                 925
ctg atc gcg cag atg gtc atc gcg ctg aag gac tcc gcc ctc ggt tac   3777
Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp Ser Ala Leu Gly Tyr
930                 935                 940                 945
cag atc ggt tat atc gag gtg gta cgc tcc ggt atc cag tcc gca tcc   3825
Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly Ile Gln Ser Ala Ser
                950                 955                 960
gtc aac cgg aac tac ctg gct gcc ctc gcg gtg gtc gcg gtc atc atg   3873
Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val Val Ala Val Ile Met
            965                 970                 975
atc ctg atc aac ttc gca ctg acc gca ctg gca gag cgt atc cag cgt   3921
Ile Leu Ile Asn Phe Ala L u Thr Ala Leu Ala Glu Arg Ile Gln Arg
        980                 985                 990
cag ctg cgt gcc gga cgt gcc cgc agg aac att gtg gca aag gtg ccc   3969
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Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile Val Ala Lys Val Pro
995 1000 1005

gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg gat 4017
Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val Asp
1010 1015 1020 1025

tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg tca ttc 4065
Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro Ser Phe
1030 1035 1040

tgacaggtcc ctggatcccc gctgcggtca ggaggcgggt gcaacaatga agtccggctg 4125
cccagatgtc tggggcagcc ggactttgtg gcagatcaat gctgactgag gtcctcgatg 4185
cgctcatcga gagcctcccg ggccaggtcc atcgacatac ccgcggggaa tccacgacgg 4245
gcaagtgct 4254

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<210> 17

<211> 242

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 17

Met Ile Lys Met Thr Gly Val Gln Lys Phe Phe Asp Asp Phe Gln Ala
1 5 10 15

Leu Thr Asp Ile Asn Leu Glu Val Pro Ala Gly Gln Val Val Val Val
20 25 30

Leu Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn
35 40 45

Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu
50 55 60

Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly
65 70 75 80

M t Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp
85 90 95
Asn Val Thr Leu Gly Pro Met Lys Val Arg Lys Met Lys Lys Ser Glu
100 105 110
Ala Asn Glu Val Ala Met Lys Leu Leu Glu Arg Val Gly Ile Ala Asn
115 120 125
Gln Ala Glu Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg
130 135 140
Val Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe
145 150 155 160
Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu
165 170 175
Asp Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val
180 185 190
Thr His Glu Met Gly Phe Ala Arg Arg Ala Ala Asp Arg Val Leu Phe
195 200 205
Met Ser Asp Gly Ala Ile Val Glu Asp Ser Asp Pro Glu Thr Phe Phe
210 215 220
Thr Asn Pro Gln Thr Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu
225 230 235 240
Ala His

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<210> 18

<211> 294

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 18

Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala

1 5 10 15

Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly

20 25 30

Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly

35 40 45

Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser

50 55 60

Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile

65 70 75 80

Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr

85 90 95

Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met

100 105 110

Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn

115 120 125

Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu

130 135 140

Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile

145 150 155 160

Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val

165 170 175

Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val

180 185 190

Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr

195 200 205

Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val

210 215 220

Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile

225 230 235 240

Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
245 250 255
Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
260 265 270
Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
275 280 285
Leu Ser Phe Leu Asp Glu
290

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<210> 19
<211> 228
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 19
Met Ser Thr Leu Trp Ala Asp Leu Gly Pro Ser Leu Leu Pro Ala Phe
1 5 10 15
Trp Val Thr Ile Gln Leu Thr Val Tyr Ser Ala Ile Gly Ser Met Ile
20 25 30
Leu Gly Thr Ile Leu Thr Ala Met Arg Val Ser Pro Val Lys Ile Leu
35 40 45
Arg Ser Ile Ser Thr Ala Tyr Ile Asn Thr Val Arg Asn Thr Pro Leu
50 55 60
Thr Leu Val Ile Leu Phe Cys Ser Phe Gly Leu Tyr Gln Asn Leu Gly
65 70 75 80
Leu Thr Leu Ala Gly Arg Asp Ser Ser Thr Phe Leu Ala Asp Asn Asn
85 90 95
Phe Arg Leu Ala Val Leu Gly Phe Ile Leu Tyr Thr Ser Ala Phe Val
100 105 110

Ala Glu Ser Leu Arg Ser Gly Ile Asn Thr Val His Phe Gly Gln Ala
115 120 125
Glu Ala Ala Arg Ser Leu Gly Leu Gly Phe Ser Asp Ile Phe Arg Ser
130 135 140
Ile Ile Phe Pro Gln Ala Val Arg Ala Ala Ile Ile Pro Leu Gly Asn
145 150 155 160
Thr Leu Ile Ala Leu Thr Lys Asn Thr Thr Ile Ala Ser Val Ile Gly
165 170 175
Val Gly Glu Ala Ser Leu Leu Met Lys Ser Thr Ile Glu Asn His Ala
180 185 190
Asn Met Leu Phe Val Val Phe Ala Ile Phe Ala Val Gly Phe Met Ile
195 200 205
Leu Thr Leu Pro Met Gly Leu Gly Leu Gly Lys Leu Ala Glu Lys Met
210 215 220
Ala Val Lys Lys
225

【００８６】

<210> 20
<211> 277
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 20
Val Gly Ser Val Leu Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp
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Thr Pro Phe Leu Asp Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly
20 25 30
Leu Trp Gly Thr Leu Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu
35 40 45

Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu
50 55 60
Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro
65 70 75 80
Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln
85 90 95
Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu
100 105 110
Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile
115 120 125
Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met
130 135 140
Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala
145 150 155 160
Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp
165 170 175
Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly
180 185 190
Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val
195 200 205
Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala
210 215 220
Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile
225 230 235 240
Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp
245 250 255
Asn Val Asn Val Asp Trp His Asp Pr Asp Tyr Lys Glu Val Lys His
260 265 270
Pr Gly Pr Ser Phe

275

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<210> 21

<211> 3598

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (454)..(3222)

<400> 21

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aaccgccggt gacacccctg ccatttgggc agctcccccc acctcaccat gtccacattt 120

tccataatgt ggcctgtaac acccttgggc tcaaggcttc cacgccccac cgggaccctc 180

atcagcaggt gaaacagacc ctcctgcaat gctttgttaa aaagaaccgc cctttgtgcg 240

tatccttgtg tcaattgtgc gcgcactgcc accagctttc ctcaggattg aacacggtcg 300

ggaaatcctc cccggatacc ctgcacgccc cacctcccac accgacaccg gcggggaggg 360

ccgggcacgt tttcagctgc gggtgatgga agcggtcgcc ggtcccccgg tcgcataaac 420

gaaatgaaaa acattccaac aggaggtgtg gaa atg gcc gat caa gca aaa ctt 474

Met Ala Asp Gln Ala Lys Leu

1 5

ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc 522

Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly

10 15 20

gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg 570

Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp

25 30 35

atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc 618

Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala

40 45 50 55

```
cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc   666
Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val
                60                  65                  70
cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca   714
Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr
            75                  80                  85
tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac   762
Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr
        90                  95                 100
cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag   810
Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln
    105                 110                 115
cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc   858
Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala
120                 125                 130                 135
gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac   906
Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp
                140                 145                 150
cac ccg ggt ggc ggt gac cag gtc ttc ttc cag ggt cac gcc tcc ccg   954
His Pro Gly Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro
            155                 160                 165
ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat  1002
Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp
        170                 175                 180
ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg  1050
Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro
    185                 190                 195
tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc  1098
Ser Tyr Pro His Pr  His Gly Met Pr  Asp Phe Trp Glu Phe Pro Thr
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200 205 210 215

gtg tcc atg ggc ctc ggg ccc atg gat gcc atc tac cag gcg cgc ttc 1146
Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg Phe
220 225 230

aac cgc tac ctg cac aac cgt ggc atc aag gac acc tcg gag cag cac 1194
Asn Arg Tyr Leu His Asn Arg Gly Ile Lys Asp Thr Ser Glu Gln His
235 240 245

gtc tgg gca ttc ctc ggt gac ggc gag atg gat gag ccg gag tcc cgt 1242
Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Arg
250 255 260

ggt ctc atc cac cag gct gcg ctg aac aac ctg gac aac ctc acc ttc 1290
Gly Leu Ile His Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr Phe
265 270 275

gtg atc aac tgc aac ctg cag cgt ctt gat ggc ccg gtc cgc ggt aac 1338
Val Ile Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly Asn
280 285 290 295

acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggt gcc ggc tgg 1386
Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly Trp
300 305 310

tcc gtc atc aag gtc atc tgg ggc cgt gag tgg gat gaa ctg ctg gag 1434
Ser Val Ile Lys Val Ile Trp Gly Arg Glu Trp Asp Glu Leu Leu Glu
315 320 325

aag gac cag gac ggt gct ctt gtc gag gtc atg aac aac acc tcc gac 1482
Lys Asp Gln Asp Gly Ala Leu Val Glu Val Met Asn Asn Thr Ser Asp
330 335 340

ggt gac tac cag acc ttc aag gcc aat gac ggt gcc tac gtc cgt gag 1530
Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg Glu
345 350 355

cac ttc ttc ggc cgt gac ccc cgc acc ctc aag ctc gtc gag gac atg 1578

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His Phe Phe Gly Arg Asp Pro Arg Thr Leu Lys Leu Val Glu Asp Met
360                 365                 370                 375
acc gac gag gag atc tgg aag ctg ccc cgt ggt ggc cat gac tac cgt   1626
Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg
                380                 385                 390
aag gtc tac gcc gcc tac aag cgt gcg ctg gag acc aag gac cgc ccg   1674
Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro
            395                 400                 405
acc gtc att ctc gcc cat acc atc aag ggc tac ggc ctg ggc cac aac   1722
Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His Asn
        410                 415                 420
ttc gag ggc cgc aac gcg acc cac cag atg aag aag ctg acc ctg gat   1770
Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp
    425                 430                 435
gac ctg aag ctg ttc cgt gac aag cag ggt ctg ccc atc acc gat gag   1818
Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Leu Pro Ile Thr Asp Glu
440                 445                 450                 455
gag ctg gag aag gat ccc tac ctg cct ccg tac tac cac ccg ggt gag   1866
Glu Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu
                460                 465                 470
gac gca ccg gag atc aag tac atg aag gag cgt cgc cag gcg ctc ggt   1914
Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Gln Ala Leu Gly
            475                 480                 485
ggt ttc ctg ccg gag cgc cgt gag aag tac gag cca ctg cag gtt ccc   1962
Gly Phe Leu Pro Glu Arg Arg Glu Lys Tyr Glu Pro Leu Gln Val Pro
        490                 495                 500
ccg ctg gac aag ctg cgg tcc gtg cgc aag ggt tcc ggc aag cag cag   2010
Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln Gln
    505                 510                 515
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gtg gcc acc acc atg gcc acg gtg cgt acc ttc aag gaa ctc atg cgg 2058
Val Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met Arg
520 525 530 535

gac aag aac ctg gcc gac cgc ttg gtc ccg atc atc ccg gat gag gcc 2106
Asp Lys Asn Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu Ala
540 545 550

cgc acc ttc ggc ctg gac tcc tgg ttc ccg acc ctg aaa atc tac aac 2154
Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr Asn
555 560 565

ccg cac ggt cag aac tac gtg ccg gtc gac cat gac ctc atg ctg tcc 2202
Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu Ser
570 575 580

tac cgt gag gcc aag gac ggc cag atc ctg cat gag ggc atc aac gag 2250
Tyr Arg Glu Ala Lys Asp Gly Gln Ile Leu His Glu Gly Ile Asn Glu
585 590 595

gcc ggt tcc gtg gca tcg ttt atc gcc gcc gga acc tcc tac gcc acc 2298
Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala Thr
600 605 610 615

cat ggc gag gcc atg atc ccg ctg tac atc ttc tac tcg atg ttc ggc 2346
His Gly Glu Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe Gly
620 625 630

ttc cag cgc acc ggt gac ggc atc tgg gcc gca gcc gac cag atg acg 2394
Phe Gln Arg Thr Gly Asp Gly Ile Trp Ala Ala Ala Asp Gln Met Thr
635 640 645

cgt ggt ttc ctc ctg ggc gcc acc gcc ggt cgc acc acc ctg acc ggt 2442
Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly
650 655 660

gag ggc ctc cag cac atg gat ggc cac tcc ccg atc ctg gcc tcc acc 2490
Glu Gly Leu Gln His Met Asp Gly His Ser Pr Ile Leu Ala Ser Thr

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    665                 670                 675
aac ccc ggt gtg gag acc tat gac ccg gcg ttc tcc tac gag atc gcg   2538
Asn Pro Gly Val Glu Thr Tyr Asp Pro Ala Phe Ser Tyr Glu Ile Ala
680                 685                 690                 695
cac ctg gtc cac cgc ggc atc gac cgc atg tac gga ccg ggc aag ggt   2586
His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly
                700                 705                 710
gag aat gtc atc tac tac ctc acc atc tac aac gag cca acc ccg cag   2634
Glu Asn Val Ile Tyr Tyr Leu Thr Ile Tyr Asn Glu Pro Thr Pro Gln
            715                 720                 725
ccg gct gag cct gag gat ctg gac gtc gag ggc ctg cac aag ggc atc   2682
Pro Ala Glu Pro Glu Asp Leu Asp Val Glu Gly Leu His Lys Gly Ile
        730                 735                 740
tac ctc tac gac aag gcc gcc gag ggt gag ggc cat gag gcc tcg atc   2730
Tyr Leu Tyr Asp Lys Ala Ala Glu Gly Glu Gly His Glu Ala Ser Ile
    745                 750                 755
ctg gcc tcc ggc atc ggc atg cag tgg gca ctg cgc gcc cgt gac atc   2778
Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile
760                 765                 770                 775
ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tcg   2826
Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser
                780                 785                 790
tgg gtg gag ctg gcc cgc gac ggt gcc cgc cgt aac ctg gag gcg ctg   2874
Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu
            795                 800                 805
cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag ctg   2922
Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu
        810                 815                 820
aag aag ggt tcc ggc ccc tac gtc gcg gtg tcc gac ttc gcg acc gac   2970
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Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp
825 830 835

ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc 3018
Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu
840 845 850 855

ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt 3066
Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg
860 865 870

tac ttc aac atc gac gcc gag tcc atc gtc gtg gcg gtc ctg cgc ggc 3114
Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly
875 880 885

ctg gtc cgc gag ggt gtc atc gat gcc tcc gtg gcg gcg cac gcg gct 3162
Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala
890 895 900

gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac 3210
Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp
905 910 915

gca ccg atc gag tagacctgct tgtcgacgaa aaacaccccc gccccctcac 3262
Ala Pro Ile Glu
920

atgatgaggg gggcgggggt gtgctcgttt acggcgggta cagggggta tcagcccagc 3322
atcgccttat cggagagcgt cgcgcccttg atcttggcga attcctgcag cagatcccgc 3382
acggtgagct tctgcttcac ctctgcgctg gcctcataga cgatccgtcc ctcgtgcatc 3442
atgatgaggc ggttacccag gcggatagcc tgttccatgt tgtgggtgac catgagggtg 3502
gtcagtttgc cgtcctcgac gatcttctcg gtcagggtgg tgaccagttc ggctcgctgg 3562
gggtccaggg cggcggtgtg ttcgtcgaga agcatg 3598

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<210> 22

<211> 923

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 22

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 1               5                  10                  15
Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
            20                  25                  30
Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
        35                  40                  45
Asp Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
    50                  55                  60
Arg Ala Ser Ala Lys Arg Val Pro Leu Pro Pro Met Thr Ser Thr Asp
65                  70                  75                  80
Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Asp Phe Pro Gly Asp
                85                  90                  95
Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala
            100                 105                 110
Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
        115                 120                 125
Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn
    130                 135                 140
His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Val Phe
145                 150                 155                 160
Phe Gln Gly His Ala Ser Pro Gly Met Tyr Ala Arg Ala Phe Leu Glu
                165                 170                 175
Gly Arg Leu Thr Glu Ser Asp Leu Asp Ser Phe Arg Gln Glu Val Ser
            180                 185                 190
Tyr Glu Gly Gly Gly Ile Pr  Ser Tyr Pr  His Pr  His Gly Met Pr
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195 200 205

Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp

210 215 220

Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile

225 230 235 240

Lys Asp Thr Ser Glu Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu

245 250 255

Met Asp Glu Pro Glu Ser Arg Gly Leu Ile His Gln Ala Ala Leu Asn

260 265 270

Asn Leu Asp Asn Leu Thr Phe Val Ile Asn Cys Asn Leu Gln Arg Leu

275 280 285

Asp Gly Pro Val Arg Gly Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser

290 295 300

Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg

305 310 315 320

Glu Trp Asp Glu Leu Leu Glu Lys Asp Gln Asp Gly Ala Leu Val Glu

325 330 335

Val Met Asn Asn Thr Ser Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn

340 345 350

Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Pro Arg Thr

355 360 365

Leu Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Lys Leu Pro

370 375 380

Arg Gly Gly His Asp Tyr Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala

385 390 395 400

Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys

405 410 415

Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln

420 425 430

Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln
435 440 445
Gly Leu Pro Ile Thr Asp Glu Glu Leu Glu Lys Asp Pro Tyr Leu Pro
450 455 460
Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys
465 470 475 480
Glu Arg Arg Gln Ala Leu Gly Gly Phe Leu Pro Glu Arg Arg Glu Lys
485 490 495
Tyr Glu Pro Leu Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg
500 505 510
Lys Gly Ser Gly Lys Gln Gln Val Ala Thr Thr Met Ala Thr Val Arg
515 520 525
Thr Phe Lys Glu Leu Met Arg Asp Lys Asn Leu Ala Asp Arg Leu Val
530 535 540
Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
545 550 555 560
Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
565 570 575
Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Lys Asp Gly Gln Ile
580 585 590
Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala
595 600 605
Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
610 615 620
Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
625 630 635 640
Ala Ala Ala Asp Gln Met Thr Arg Gly Phe Leu Leu Gly Ala Thr Ala
645 650 655
Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His

660 665 670

Ser Pro Ile Leu Ala Ser Thr Asn Pro Gly Val Glu Thr Tyr Asp Pro

675 680 685

Ala Phe Ser Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg

690 695 700

Met Tyr Gly Pro Gly Lys Gly Glu Asn Val Ile Tyr Tyr Leu Thr Ile

705 710 715 720

Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Asp Leu Asp Val

725 730 735

Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Asp Lys Ala Ala Glu Gly

740 745 750

Glu Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly Met Gln Trp

755 760 765

Ala Leu Arg Ala Arg Asp Ile Leu Ala Glu Asp Tyr Gly Ile Arg Ala

770 775 780

Asn Ile Phe Ser Ala Thr Ser Trp Val Glu Leu Ala Arg Asp Gly Ala

785 790 795 800

Arg Arg Asn Leu Glu Ala Leu Arg Asn Pro Gly Ala Asp Val Gly Glu

805 810 815

Ala Phe Val Thr Thr Gln Leu Lys Lys Gly Ser Gly Pro Tyr Val Ala

820 825 830

Val Ser Asp Phe Ala Thr Asp Leu Pro Asn Gln Ile Arg Glu Trp Val

835 840 845

Pro Gly Asp Tyr Ile Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp

850 855 860

Thr Arg Pro Ala Ala Arg Arg Tyr Phe Asn Ile Asp Ala Glu Ser Ile

865 870 875 880

Val Val Ala Val Leu Arg Gly Leu Val Arg Glu Gly Val Ile Asp Ala

885 890 895

Ser Val Ala Ala His Ala Ala Glu Lys Tyr Lys Leu S r Asp Pro Thr
900 905 910

Ala Pro Gln Val Asp Pro Asp Ala Pro Ile Glu
915 920

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<210> 23

<211> 4013

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (319)..(3735)

<400> 23

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cggcaatggg ggtctcgggc ggggggcatt cttttcacgg caaggtggtg aaattccgca 180

ggtcactccc cggccggcgg tagagaacgg agcgaaaacg gaaagcaata cgtggttttc 240

cggactggcc gttacgatgt tctgaagagt gactgccatc acccaacagg ctggtcctcg 300

tcgaaaggaa caaaaact gtg gtt aca aca aca ccc tcc acg ctg ccg gcg 351
Val Val Thr Thr Thr Pro Ser Thr Leu Pro Ala
1 5 10

ttc aaa aag atc ctg gtg gcc aac cga ggt gaa atc gcg gtg cga gca 399
Phe Lys Lys Ile Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala
15 20 25

ttc cgc gcc gcc tac gag acc ggg gcc gca acc gtg gcc atc tac ccc 447
Phe Arg Ala Ala Tyr Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro
30 35 40

cgg gag gac cgt ggc tcc ttc cac cgc tcc ttc gcc tcc gag gcg gtg 495
Arg Glu Asp Arg Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val
45 50 55

agg atc gga acc gag ggc tca ccc gtc aag gcg tac ctc gat att gat 543
Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp
60 65 70 75

gag atc atc aac gcc gcc aag aag gtg aaa gcg gac gcg gtc tac ccg 591
Glu Ile Ile Asn Ala Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro
80 85 90

ggg tat ggt ttc ctt tcg gaa aat gcc cag ctc gcg cgt gaa tgc gcg 639
Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala
95 100 105

gag aac ggc att acc ttc atc ggt ccc acc ccg gag gtg ctc gac ctc 687
Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu
110 115 120

acg ggc gac aag tcc aag gct gtg tcc gcc gcg aag aag gcc ggg ctg 735
Thr Gly Asp Lys Ser Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu
125 130 135

ccg gtg ctg gcg gaa tcc acc ccc agc acc gac atc gat gag atc gtc 783
Pro Val Leu Ala Glu Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val
140 145 150 155

aag agt gcc gag ggg cag acc tac ccg atc ttc gtc aag gcc gtc gca 831
Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala
160 165 170

ggt ggt ggc ggg cgt ggt atg cgg ttc gtc gag aag ccc gag gac ctg 879
Gly Gly Gly Gly Arg Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu
175 180 185

cgt gag ctg gcc agg gag gcc tcc cgc gag gcg gag gcc gct ttc ggt 927
Arg Glu Leu Ala Arg Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly

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        190                 195                 200
gac gga tcc gtc tac gtc gaa cgg gcc gtg atc aaa ccc cag cac atc   975
Asp Gly Ser Val Tyr Val Glu Arg Ala Val Ile Lys Pro Gln His Ile
    205                 210                 215
gag gtg cag atc ctc ggt gat cac acc ggc gat gtc atc cac ctg tat   1023
Glu Val Gln Ile Leu Gly Asp His Thr Gly Asp Val Ile His Leu Tyr
220                 225                 230                 235
gaa cgc gac tgt tcc ctg cag cgc cgc cac cag aag gtc gtg gag atc   1071
Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile
                240                 245                 250
gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc   1119
Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala
            255                 260                 265
gat gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc   1167
Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr
        270                 275                 280
gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg   1215
Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met
    285                 290                 295
aac ccc cgc atc cag gtg gaa cac acc gtg acc gag gag gtc acc tcc   1263
Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser
300                 305                 310                 315
gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg   1311
Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu
                320                 325                 330
aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc   1359
Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala
            335                 340                 345
ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc   1407
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Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro
350 355 360

gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gcg ggt gtg 1455
Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val
365 370 375

cgt ctc gac ggc gca gcc cag ctc ggc ggc gag atc acc gca cat ttc 1503
Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe
380 385 390 395

gat tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc 1551
Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr
400 405 410

gcc gtg tcc cga gcc cag cgc gcc ctg gcg gag ttc aac gtc tcc ggc 1599
Ala Val Ser Arg Ala Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly
415 420 425

gtg gcc acc aac atc ggc ttc ctg cgt gcg ctg ctg cgc gag gaa gac 1647
Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp
430 435 440

ttc acc aag agg cgc atc gac acc ggc ttc atc ggc tcc cac cag cac 1695
Phe Thr Lys Arg Arg Ile Asp Thr Gly Phe Ile Gly Ser His Gln His
445 450 455

ctg ctc cag gcc cca ccg gcc gac gat gag cag ggg cgg atc ctg gaa 1743
Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu
460 465 470 475

tac ctg gcg gat gtc acc gtg aac aaa ccc cac ggt gaa cgc ccc gag 1791
Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu
480 485 490

aca gcc cgt ccg ata gag aag ctg ccc gag gtg gag aac atc ccg ctg 1839
Thr Ala Arg Pro Ile Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu
495 500 505

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Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly
            815                 820                 825
cgc gtt tac cgc cac gag atc ccc ggc ggt cag ctg tcc aac ctg cgt   2847
Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg
        830                 835                 840
gcc cag gcc gtt gca ctg ggt ctg gcc gac cgc ttc gag ctc atc gag   2895
Ala Gln Ala Val Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu
    845                 850                 855
gac tac tac gcg gcc gtc aac gag atg ctg ggt cgt ccg acc aag gtc   2943
Asp Tyr Tyr Ala Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val
860                 865                 870                 875
acc ccg tcc tcc aag gtt gtc ggt gac ctc gca ctg cac ctc gtc ggt   2991
Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly
                880                 885                 890
gcc ggt gtg agc ccg gag gat ttc gcc gcc gat ccg cag aag tac gac   3039
Ala Gly Val Ser Pro Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp
            895                 900                 905
atc ccc gat tcg gtc atc gcc ttc ctc cgc ggc gaa ctg ggt acc cct   3087
Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro
        910                 915                 920
ccc ggt ggc tgg ccc gaa ccg ctg cgc acc cgt gca ctc gag ggt cgc   3135
Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg
    925                 930                 935
tcc cag ggt aag gcc ccg ctg gcg gag atc ccc gcc gag gag cag gcc   3183
Ser Gln Gly Lys Ala Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala
940                 945                 950                 955
cac ctg gat tcc gat gat tcc gcg gag cgt cgc ggc acc ctc aac cgc   3231
His Leu Asp Ser Asp Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg
                960                 965                 970
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ctg ctg ttc ccg aag ccg acc gag gag ttc ctt gag cac cgt cgc cgc 3279
Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg
975 980 985

ttc ggc aac acc tcc gcc ctg gat gac cgc gag ttc ttc tac ggc ttg 3327
Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu
990 995 1000

aag gag gga cgt gag gag ctg atc cga ctg acc ggt gtg tcc acc ccg 3375
Lys Glu Gly Arg Glu Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro
1005 1010 1015

atg gtg gtc cgc ctg gat gcg gtg tcc gaa ccg gat gac aaa ggc atg 3423
Met Val Val Arg Leu Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met
1020 1025 1030 1035

cgc aac gtg gtg gtc aac gtc aac ggc cag atc cgc ccg atc aag gtg 3471
Arg Asn Val Val Val Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val
1040 1045 1050

cgc gac cgt tcc gtg gag tcc gtc acc gcc acc gcg gag aag gcc gat 3519
Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp
1055 1060 1065

gcc acc aac aag ggc cat gtc gcc gca cca ttc gcc ggt gtg gtc acc 3567
Ala Thr Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr
1070 1075 1080

gtg acc gtc gcc gag ggt gat gag atc aag gct ggc gac gcc gtg gcc 3615
Val Thr Val Ala Glu Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala
1085 1090 1095

atc att gag gcc atg aag atg gag gcc acc atc acc gcg cct gtc gac 3663
Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp
1100 1105 1110 1115

ggt gtc atc gac cgc gtc gtg gtg ccc gcc gcc acc aag gtc gag ggc 3711
Gly Val Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly

1120 1125 1130

ggc gac ctc atc gtg gtc gtg tcc tagcgactga gagccacaac ccgtcccggg 3765
Gly Asp Leu Ile Val Val Val Ser

1135

tgccttgtta tcaacctccc cctgatgatg ttctcagggg gaggctctac gtacctcacc 3825
gtgacggtgc atgtatatcg tcctgctgga gagaatgctc caggtaggaa cgccaaccac 3885
cccactccgt gatgtcccgt gctgatccca ggcaggccgg ttggaaagaa aaaccagtga 3945
tggaacggcc atcggacagc gagacggaac caagcgtcat cggctccggt agagcggtga 4005
ggagcctg 4013

【００９０】

<210> 24

<211> 1139

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 24

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20 25 30
Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
35 40 45
Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
50 55 60
Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Asn Ala
65 70 75 80
Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu
85 90 95
Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
100 105 110

Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
115 120 125
Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
130 135 140
Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
145 150 155 160
Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
165 170 175
Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu Arg Glu Leu Ala Arg
180 185 190
Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val Tyr
195 200 205
Val Glu Arg Ala Val Ile Lys Pro Gln His Ile Glu Val Gln Ile Leu
210 215 220
Gly Asp His Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser
225 230 235 240
Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
245 250 255
Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
260 265 270
Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
275 280 285
Asp Glu Ala Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln
290 295 300
Val Glu His Thr Val Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys
305 310 315 320
Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu
325 330 335
Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala Leu Gln Cys Arg Ile

340 345 350

Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro Asp Thr Gly Val Ile

355 360 365

Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala

370 375 380

Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val

385 390 395 400

Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ser Arg Ala

405 410 415

Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly Val Ala Thr Asn Ile

420 425 430

Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Lys Arg Arg

435 440 445

Ile Asp Thr Gly Phe Ile Gly Ser His Gln His Leu Leu Gln Ala Pro

450 455 460

Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu Tyr Leu Ala Asp Val

465 470 475 480

Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu Thr Ala Arg Pro Ile

485 490 495

Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu Pro Arg Gly Ser Arg

500 505 510

Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe Ala Arg Asp Leu Arg

515 520 525

Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His

530 535 540

Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Thr Pro Ala

545 550 555 560

Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala

565 570 575

Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp
580 585 590
Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn
595 600 605
Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr
610 615 620
Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu Ala Ala Lys Ser Gly
625 630 635 640
Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Ile Ser Gln Met
645 650 655
Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly Thr Ser Val Ala Glu
660 665 670
Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn Pro Gly Glu Lys Leu
675 680 685
Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu Gln Ile Val Asp Ser
690 695 700
Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Arg
705 710 715 720
Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu
725 730 735
Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr
740 745 750
Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala Val Asp Ala Ala Ser
755 760 765
Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Met Ser Ala Leu Val
770 775 780
Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Asn Leu Gln Ala
785 790 795 800
Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu

805 810 815

Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His

820 825 830

Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Val Ala

835 840 845

Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala

850 855 860

Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys

865 870 875 880

Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Ser Pro

885 890 895

Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val

900 905 910

Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro Pro Gly Gly Trp Pro

915 920 925

Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Gln Gly Lys Ala

930 935 940

Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala His Leu Asp Ser Asp

945 950 955 960

Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg Leu Leu Phe Pro Lys

965 970 975

Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser

980 985 990

Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Lys Glu Gly Arg Glu

995 1000 1005

Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro Met Val Val Arg Leu

1010 1015 1020

Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Val

025 1030 1035 1040

Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val Arg Asp Arg Ser Val
1045 1050 1055
Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ala Thr Asn Lys Gly
1060 1065 1070
His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu
1075 1080 1085
Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met
1090 1095 1100
Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp Gly Val Ile Asp Arg
105 1110 1115 1120
Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val
1125 1130 1135
Val Val Ser

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<211> 3306

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (64)..(2820)

<400> 25

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acc gtg aat gaa ctt ctc cgt gac gat atc cgt tat ctc ggc cgg atc 108
Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile
1 5 10 15

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ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg   156
Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu
                20                  25                  30
gtt gaa cgc gcc cgc cgg acc tcc ttc gac atc gcc aag gga cgc gcg   204
Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala
            35                  40                  45
gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac   252
Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp
        50                  55                  60
gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac   300
Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn
    65                  70                  75
ctc gcg gag gat ttg cat gac gca gcc cag cgg gaa cag gcc ctg aac   348
Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn
80                  85                  90                  95
tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa   396
Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys
                100                 105                 110
ctg gat gat gcc ggg gtg ggc agc ggt gag gtc gcc gcg gtg atc cgc   444
Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg
            115                 120                 125
aat gcg ctc gtc gcc ccg gtg ctc acc gcg cac ccg acg gaa acc cga   492
Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg
        130                 135                 140
cgt cgt acc gtg ttc gac gcg cag aag cac atc acc gcc ctg atg gag   540
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu
    145                 150                 155
gaa cgc cac ctc ctc ctg gcg ctg ccc acg cat gcc cgg acc cag tcc   588
Glu Arg His Leu Leu Leu Ala Leu Pr  Thr His Ala Arg Thr Gln Ser
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160 165 170 175

aag ctg gat gac atc gag cgc aac atc cgg cga cgg atc acg atc ctg 636
Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu
180 185 190

tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag 684
Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu
195 200 205

gtc gag gtt gga ctg cgc tac tac aag ctc agc ctg ttg gcc gag atc 732
Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile
210 215 220

ccc cgc atc aat cat gat gtg acc gtg gaa ctg gcc cgg cgt ttc ggc 780
Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly
225 230 235

ggg gat atc ccc acc acg gcg atg gtc agg ccg gga tcc tgg atc ggc 828
Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly
240 245 250 255

ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac 876
Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr
260 265 270

gcc acc cat cgg gcc gcg gag acc gtg ctc aag tac tac gtc aag caa 924
Ala Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln
275 280 285

ctg cac gcc ctg gaa cac gaa ctc agt ctc tcc gac cgg atg aac gtc 972
Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val
290 295 300

atc agc gat gag ctg cgt gtg ctt gcc gat gcc ggc cag aat gac atg 1020
Ile Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met
305 310 315

ccc agc cgg gtt gat gaa ccc tac cgg cgg gcc atc cac ggc atg cgt 1068

```
Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg
320                 325                 330                 335
ggc cgg atg ctg gcc acc acg gcc gcc ctg atc ggt gag gag gcg gtc   1116
Gly Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val
                340                 345                 350
---gag-ggc-acc-tgg-ttc-aag-acc-ttc-acg-ccc-tat-acc-gat acc-cac gag   1164
Glu Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu
            355                 360                 365
ttc aaa cgc gac ctc gat atc gtg gat ggt tcc ctg aga atg tcc cgg   1212
Phe Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg
        370                 375                 380
gat gac atc atc gcc gat gac cgt ctg gcc atg ctg cgc tcg gcc ctg   1260
Asp Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu
    385                 390                 395
gac agc ttc ggg ttc aac ctc tac tcc ctg gat ctg cgc cag aat tcc   1308
Asp Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser
400                 405                 410                 415
gac ggt ttc gag gat gtc ctc acc gaa ttg ttc gcc acc gcc cag acc   1356
Asp Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr
                420                 425                 430
gag aag aac tac cgc ggg ttg acg gag gcg gag aag ctg gac ctg ctg   1404
Glu Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu
            435                 440                 445
atc cgc gaa ctg agc aca ccc cgc ccg ctc atc ccg cac ggg gac ccg   1452
Ile Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro
        450                 455                 460
gac tac tcc gag gcc acc aac cgt gaa ctg ggg att ttt tcg aag gcc   1500
Asp Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala
    465                 470                 475
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gcg gag gcc gtg cgt aaa ttc ggt cct ctc atg gtg ccg cac tgc atc 1548
Ala Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile
480 485 490 495
atc tcc atg gcc tct tcc gtc acg gac atc ctc gaa ccg atg gtg ctg 1596
Ile Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu
500 505 510
ctc aag gag ttc ggt ctg atc cgg gcc aac ggg aag aac ccg acg ggc 1644
Leu Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly
515 520 525
agc gtc gac gtg atc ccg ctg ttc gag acg atc gat gac ctc cag cgt 1692
Ser Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg
530 535 540
ggc gcg ggc atc ctg gag gaa ttg tgg gac atc gac ctc tac cgc aat 1740
Gly Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn
545 550 555
tac ctt gag cag cgg gac aac gtc cag gag gtc atg ctg ggg tat tcc 1788
Tyr Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser
560 565 570 575
gac tcc aac aag gac ggc ggg tac ttc gcc gcc aac tgg gcg ctt tac 1836
Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr
580 585 590
gac gcg gag tta cgc ctg gtc gaa cta tgc cgg ggc cgt aat gtc aag 1884
Asp Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys
595 600 605
ctc cgt ctc ttc cac ggt cgt ggt ggc acg gtg ggt cgt ggc ggt ggc 1932
Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly
610 615 620
ccc tcc tat gat gcg atc ctg gcc cag ccc aag ggc gcg gtc cgg ggt 1980
Pr Ser Tyr Asp Ala Ile Leu Ala Gln Pr Lys Gly Ala Val Arg Gly

625 630 635

gcg gtg cgg gtg act gaa cag ggc gag atc atc tcc gcg aag tac ggt 2028
Ala Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly
640 645 650 655

aac ccg gat acg gca cgc cgc aac ctt gag gcc ctg gtg tcc gcg acg 2076
Asn Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr
660 665 670

ctg gag gca tcg ctt ctg gat gat gtg gaa ctg ccc aat cgg gaa cgc 2124
Leu Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg
675 680 685

gcg cac cag atc atg ggg gag atc tcg gag ttg agc ttc cgc agg tac 2172
Ala His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr
690 695 700

tca tca ctg gtc cat gag gat ccc gga ttc atc cag tac ttc acc cag 2220
Ser Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln
705 710 715

tcc acc ccc ctg cag gag atc gga tcc ctc aac atc ggt tcc cga ccc 2268
Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro
720 725 730 735

tcc tca cgt aaa cag acc aac acg gtg gag gat ctg cgt gcc atc ccg 2316
Ser Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro
740 745 750

tgg gtg ctc agc tgg tcc cag tcc cgt gtc atg ctg ccg ggc tgg ttc 2364
Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe
755 760 765

ggt gtg ggt acc gca ctg cgt gag tgg atc ggt gag ggg gag ggg gct 2412
Gly Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala
770 775 780

gcg gag cgc atc gcg gag ctg cag gaa ctc aac cgg tgc tgg ccg ttc 2460

Ala Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe
785 790 795

ttc acc tcg gtg ctg gac aac atg gcc cag gtg atg agc aag gcg gaa 2508
Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu
800 805 810 815

ctg cgc ctg gcc agg ttg tac gcc gat ctc atc ccg gat cgc gag gtg 2556
Leu Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val
820 825 830

gcg gac cgg atc tat gag acc atc ttc ggg gag tat ttc ctg acc aag 2604
Ala Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys
835 840 845

gag atg ttc tgc acc atc acc ggt tcc cag gac ctg ctc gat gac aac 2652
Glu Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn
850 855 860

ccg gcg ctg gcg cga tcg gtg cgc agt cgg ttc ccg tac ctg ctg ccg 2700
Pro Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro
865 870 875

ctc aat gtc atc cag gtg gag atg atg cgc cgg tac cgg tcc ggt gat 2748
Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp
880 885 890 895

gag ggc acg gct gtc cca cgt aat atc cgc ctg acc atg aat gga ttg 2796
Glu Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu
900 905 910

tcc acg gcc ctg cgc aac tcg ggt tagggcgcca gacgccccgg gaacccgcac 2850
Ser Thr Ala Leu Arg Asn Ser Gly
915

cctgtgtata ctgtctaaag ttgcccggtg tcatccgggc gtgatggata gacaacttaa 2910

cggcaaagga ttctccccac atggcactga cgcttcaaat cgtcctcgtt ctcgccagcg 2970

tgctcatgac ggtcttcgtc ctgctgcaca agggtaaggg cggaggtctg tcaagcctct 3030

tcggtggtgg cgtccagtcc aacctctccg gttccacggt ggtggagaag aacctggacc 3090
gcgtcaccat cctgaccgca gtcatctggt tgatctgcat tgtcgcgctc aacctcatcc 3150
aggcgtactc ctagcacctg atctttcaag gcctgccctt cggggcaggc ctttttgca 3210
ttctccaggt gatgtccatc acccaccggt tttaaactat tgaccgatag aaacacctgc 3270
actaggttat ctgttatgca atagaaaata gtgcat 3306

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<210> 26
<211> 919
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 26

Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile Leu
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Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu Val
20 25 30
Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala Glu
35 40 45
Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala
50 55 60
Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu
65 70 75 80
Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser
85 90 95
Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu
100 105 110
Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn
115 120 125
Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg

130 135 140

Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala L u Met Glu Glu

145 150 155 160

Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys

165 170 175

Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp

180 185 190

Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val

195 200 205

Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro

210 215 220

Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly

225 230 235 240

Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly

245 250 255

Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala

260 265 270

Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu

275 280 285

His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile

290 295 300

Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro

305 310 315 320

Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg Gly

325 330 335

Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu

340 345 350

Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe

355 360 365

Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp
370 375 380
Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp
385 390 395 400
Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp
405 410 415
Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
420 425 430
Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile
435 440 445
Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp
450 455 460
Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala
465 470 475 480
Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
485 490 495
Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu
500 505 510
Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser
515 520 525
Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg Gly
530 535 540
Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn Tyr
545 550 555 560
Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp
565 570 575
Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr Asp
580 585 590
Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys Leu

595 600 605

Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pr

610 615 620

Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly Ala

625 630 635 640

Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn

645 650 655

Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu

660 665 670

Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg Ala

675 680 685

His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr Ser

690 695 700

Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln Ser

705 710 715 720

Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser

725 730 735

Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro Trp

740 745 750

Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly

755 760 765

Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala Ala

770 775 780

Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe Phe

785 790 795 800

Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu

805 810 815

Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val Ala

820 825 830

Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys Glu
835 840 845

Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn Pro
850 855 860

Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro Leu
865 870 875 880

Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp Glu
885 890 895

Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu Ser
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Thr Ala Leu Arg Asn Ser Gly
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<211> 3907

<212> DNA

<213> Corynebacterium thermoaminogenes

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<221> CDS

<222> (686)..(3388)

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ttattattag ctggtggcgg agatggaact aaagctctca acgcaattca gagtgccgct 180

attattagtg cgtttccatt ctcctttgtc gtcatattaa tgatgatcag tttctacaaa 240

gatgctaata aagaacgtaa attcttagga ttaacattaa cgcctaataa acacagatta 300

gaagaatacg ttaaatatca acaagaggat tacgaatctg atattttaga aaaacgtgaa 360

tctagacgta atcgtgaaag agaagaataa ttgaatgaaa tatctactat aatggtgggt 420

ttaaagctat caacaatttt gttgatagct atttttatgt ttcaaacata taaatattat 480

ttacttgcga ttgataacca ttctcaatta ataaaaataa cttatagtac aaatgcgtta 540

taataagttt tacttatact acctgattaa aaatgcgaaa tgaaaaatga ccccctttata 600

tacctataca gttgtgttcg aaaacatata ataatacaat ttaactaagg catataaata 660

tatagaaatt caaggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712

Met Ala Ser Asn Phe Lys Glu Thr Ala

1 5

aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760

Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu

10 15 20 25

aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808

Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr

30 35 40

tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856

Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe

45 50 55

gta att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904

Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys

60 65 70

ggt aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952

Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln

75 80 85

gac ttc act ggt gta cca gca gta gtt gac tta gcg tct tta cgt aaa 1000

Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys

90 95 100 105

gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gta 1048

Ala Met Asn Asp Val Gly Gly Asp Il Asn Lys Il Asn Pro Glu Val

110 115 120

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cca gtt gac tta gtt att gac cac tct gta caa gta gat agt tat gct   1096
Pro Val Asp Leu Val Ile Asp His S r Val Gln Val Asp S r Tyr Ala
            125                 130                 135
aat cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac   1144
Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn
        140                 145                 150
tat gaa cgt tac caa ttc tta aac tgg gca aca aaa gca ttt gat aac   1192
Tyr Glu Arg Tyr Gln Phe Leu Asn Trp Ala Thr Lys Ala Phe Asp Asn
    155                 160                 165
tat aat gca gta cca cct gct aca ggt att gtc cac caa gta aac tta   1240
Tyr Asn Ala Val Pro Pro Ala Thr Gly Ile Val His Gln Val Asn Leu
170                 175                 180                 185
gaa tac tta gcg aat gtt gta cat gtt cgt gac gtt gac gga gaa caa   1288
Glu Tyr Leu Ala Asn Val Val His Val Arg Asp Val Asp Gly Glu Gln
                190                 195                 200
act gct ttc cca gat aca tta gtt ggt act gac tca cat act aca atg   1336
Thr Ala Phe Pro Asp Thr Leu Val Gly Thr Asp Ser His Thr Thr Met
            205                 210                 215
att aac ggt att ggt gta tta ggt tgg ggt gtc ggc ggt atc gaa gct   1384
Ile Asn Gly Ile Gly Val Leu Gly Trp Gly Val Gly Gly Ile Glu Ala
        220                 225                 230
gaa gca ggt atg tta gga caa cca tca tac ttc cca att cca gaa gtt   1432
Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pro Glu Val
    235                 240                 245
att ggt gtt aaa tta agt aat gaa tta cca caa ggt tca aca gca act   1480
Ile Gly Val Lys Leu Ser Asn Glu Leu Pr  Gln Gly Ser Thr Ala Thr
250                 255                 260                 265
gac tta gca tta cgt gta act gaa gag tta cgt aaa cgt ggt gta gta   1528
Asp Leu Ala Leu Arg Val Thr Glu Glu Leu Arg Lys Arg Gly Val Val
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270 275 280

ggt aaa ttc gtt gag ttc ttt ggt cct ggt gta aca aac tta cca tta 1576
Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Thr Asn Leu Pro Leu

285 290 295

gct gac cgt gca aca att gcg aac atg gcg cct gaa tat ggt gca act 1624
Ala Asp Arg Ala Thr Ile Ala Asn Met Ala Pro Glu Tyr Gly Ala Thr

300 305 310

tgt ggt ttc ttc cca gtt gat gaa gaa tca ctt aaa tac atg aaa tta 1672
Cys Gly Phe Phe Pro Val Asp Glu Glu Ser Leu Lys Tyr Met Lys Leu

315 320 325

act ggt cgt aaa gat gat cat att gca cta gta aaa gaa tat tta caa 1720
Thr Gly Arg Lys Asp Asp His Ile Ala Leu Val Lys Glu Tyr Leu Gln

330 335 340 345

caa aat aat atg ttc ttc caa gtt gaa aat gaa gat cct gaa tat act 1768
Gln Asn Asn Met Phe Phe Gln Val Glu Asn Glu Asp Pro Glu Tyr Thr

350 355 360

gaa gtg att gat tta gat tta tct aca gtt caa gct tct tta tca ggt 1816
Glu Val Ile Asp Leu Asp Leu Ser Thr Val Gln Ala Ser Leu Ser Gly

365 370 375

cca aaa cgt cca caa gat tta atc ttc tta agt gac atg aaa act gaa 1864
Pro Lys Arg Pro Gln Asp Leu Ile Phe Leu Ser Asp Met Lys Thr Glu

380 385 390

ttc gaa aaa tca gtt aca gca cca gct ggt aac caa ggt cac ggt tta 1912
Phe Glu Lys Ser Val Thr Ala Pro Ala Gly Asn Gln Gly His Gly Leu

395 400 405

gat gaa agt gaa ttt gat aag aaa gca gaa atc aaa ttt aat gat ggt 1960
Asp Glu Ser Glu Phe Asp Lys Lys Ala Glu Ile Lys Phe Asn Asp Gly

410 415 420 425

aga act tca act atg aag act ggt gat gtt gcg att gca gcg att aca 2008

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Arg Thr Ser Thr Met Lys Thr Gly Asp Val Ala Ile Ala Ala Ile Thr
                430                 435                 440
tca tgt aca aat aca tct aac cct tac gtt atg tta ggt gca ggt tta  2056
Ser Cys Thr Asn Thr Ser Asn Pro Tyr Val Met Leu Gly Ala Gly Leu
            445                 450                 455
gta gct aaa aaa gca att gaa aaa ggc tta aaa gta cct gat tat gta  2104
Val Ala Lys Lys Ala Ile Glu Lys Gly Leu Lys Val Pro Asp Tyr Val
        460                 465                 470
aaa act tca tta gca cca ggt tca aaa gtt gtt act gga tat tta aga  2152
Lys Thr Ser Leu Ala Pro Gly Ser Lys Val Val Thr Gly Tyr Leu Arg
    475                 480                 485
gat tca ggt tta caa gaa tat ctt gat gac tta ggt ttc aac tta gtt  2200
Asp Ser Gly Leu Gln Glu Tyr Leu Asp Asp Leu Gly Phe Asn Leu Val
490                 495                 500                 505
ggt tat ggt tgt aca act tgt atc ggt aac tca ggt cca tta tta cct  2248
Gly Tyr Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Leu Pro
                510                 515                 520
gaa att gaa aaa gca gta gct gac gaa gat tta tta gta act tct gta  2296
Glu Ile Glu Lys Ala Val Ala Asp Glu Asp Leu Leu Val Thr Ser Val
            525                 530                 535
ctt tct ggt aac cgt aac ttt gaa ggt cgt atc cat ccg tta gtt aaa  2344
Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile His Pro Leu Val Lys
        540                 545                 550
gct aac tac tta gct tca cca caa tta gtt gta gct tat gca tta gct  2392
Ala Asn Tyr Leu Ala Ser Pro Gln Leu Val Val Ala Tyr Ala Leu Ala
    555                 560                 565
gga acg gtt gat atc gat tta cac aat gaa cct atc ggt aaa ggt aaa  2440
Gly Thr Val Asp Ile Asp Leu His Asn Glu Pro Ile Gly Lys Gly Lys
570                 575                 580                 585
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gat ggc gaa gat gta tac ctt aaa gat atc tgg cca agt atc aaa gaa   2488
Asp Gly Glu Asp Val Tyr Leu Lys Asp Ile Trp Pro Ser Ile Lys Glu
                590                 595                 600

gtt gca gac act gtt gat agt gtc gta acg cca gaa tta ttc tta gaa   2536
Val Ala Asp Thr Val Asp Ser Val Val Thr Pro Glu Leu Phe Leu Glu
            605                 610                 615

gaa tat gca aat gta tac gaa aat aat gaa atg tgg aat gaa atc gac   2584
Glu Tyr Ala Asn Val Tyr Glu Asn Asn Glu Met Trp Asn Glu Ile Asp
        620                 625                 630

gtt act gac gca cca tta tat gat ttc gat cca aat tca act tat att   2632
Val Thr Asp Ala Pro Leu Tyr Asp Phe Asp Pro Asn Ser Thr Tyr Ile
    635                 640                 645

caa aat cca tca ttc ttc caa ggt tta tct aaa gaa cca gga act att   2680
Gln Asn Pro Ser Phe Phe Gln Gly Leu Ser Lys Glu Pro Gly Thr Ile
650                 655                 660                 665

gaa cca tta aaa gat tta cgt att atg ggt aaa ttt ggt gat tca gtt   2728
Glu Pro Leu Lys Asp Leu Arg Ile Met Gly Lys Phe Gly Asp Ser Val
                670                 675                 680

aca act gac cac att tct cca gca ggt gcg atc ggt aaa gat aca cca   2776
Thr Thr Asp His Ile Ser Pro Ala Gly Ala Ile Gly Lys Asp Thr Pro
            685                 690                 695

gca ggt aaa tat tta tta gac cat gat gtt cca att aga gaa ttt aac   2824
Ala Gly Lys Tyr Leu Leu Asp His Asp Val Pro Ile Arg Glu Phe Asn
        700                 705                 710

tct tat ggt tca aga cgt ggt aac cat gaa gta atg gta cgt ggt act   2872
Ser Tyr Gly Ser Arg Arg Gly Asn His Glu Val Met Val Arg Gly Thr
    715                 720                 725

ttc gct aat atc cgt att aaa aac caa tta gca cca ggc act gaa ggt   2920
Phe Ala Asn Ile Arg Ile Lys Asn Gln Leu Ala Pro Gly Thr Glu Gly
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730 735 740 745

gga ttt aca aca tat tgg cct aca gaa gaa atc atg cct atc tat gat 2968
Gly Phe Thr Thr Tyr Trp Pro Thr Glu Glu Ile Met Pro Ile Tyr Asp
750 755 760

gca gct atg aga tac aaa gaa aat ggt act ggt tta gct gtt tta gct 3016
Ala Ala Met Arg Tyr Lys Glu Asn Gly Thr Gly Leu Ala Val Leu Ala
765 770 775

ggt aat gat tac ggt atg ggt tca tct cgt gac tgg gca gct aaa ggt 3064
Gly Asn Asp Tyr Gly Met Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly
780 785 790

act aac tta tta ggt gtt aaa act gtt att gca caa agt tat gaa cgt 3112
Thr Asn Leu Leu Gly Val Lys Thr Val Ile Ala Gln Ser Tyr Glu Arg
795 800 805

atc cat cgt tca aac tta gta atg atg ggt gta tta cca tta caa ttt 3160
Ile His Arg Ser Asn Leu Val Met Met Gly Val Leu Pro Leu Gln Phe
810 815 820 825

aaa caa ggt gag tca gct gat tct cta ggt tta gaa ggt aaa gaa gaa 3208
Lys Gln Gly Glu Ser Ala Asp Ser Leu Gly Leu Glu Gly Lys Glu Glu
830 835 840

att tct gta gat atc gat gaa aat gtt aaa cca cat gat tta gta act 3256
Ile Ser Val Asp Ile Asp Glu Asn Val Lys Pro His Asp Leu Val Thr
845 850 855

gtt cat gct aaa aaa gaa aac gga gaa gtt gtt gat ttt gaa gca atg 3304
Val His Ala Lys Lys Glu Asn Gly Glu Val Val Asp Phe Glu Ala Met
860 865 870

gtt cgt ttc gat tca tta gta gaa tta gat tat tat cgt cat ggt ggt 3352
Val Arg Phe Asp Ser Leu Val Glu Leu Asp Tyr Tyr Arg His Gly Gly
875 880 885

atc tta caa atg gta tta aga aac aaa tta gct caa taatcacaat 3398

Ile Leu Gln Met Val Leu Arg Asn Lys Leu Ala Gln

890 895 900

gtgacttttg acagtgctaa cgtttaggtt agcactgttt ttttatgcta aactatatat 3458

gtaatgttaa tagttaagga aggattggac ttaaatgatt tatagtttga ctgaaattga 3518

accaagatat caagagacag ataaaatggg cgtgatttat catggcaatt atgcaacatg 3578

gtttgaagta gcgcgtacag attacattag aaaactagga tttagttatg ctgatatgga 3638

aaagcaaggg atcatttctc cagttacaga cttaaatatc aaatataaaa aatcaatttt 3698

ttatcctgaa aaagtaacca ttaaaacatg ggtggaaaaa tattcaagat tacgttctgt 3758

gtatagatat gaaattttta atgaacaggg agaacttgca actacaggtt atactgagtt 3818

aatttgtatg aaagctgata cctttagacc aattagatta gatcgttatt tctcagattg 3878

gcatgaaacc tatagtaaag ttgaagctt 3907

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<212> PRT

<213> Corynebacterium thermoaminogenes

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35 40 45

Ser Val Leu Arg Gln Glu Asp Asp Phe Val Ile Thr Asp Asp His Ile

50 55 60

Lys Gln Leu Ala Glu Phe Gly Lys Lys Gly Asn Glu Gly Glu Val Pr

65 70 75 80

Phe Lys Pr Ser Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pr Ala

85 90 95

Val Val Asp Leu Ala Ser Leu Arg Lys Ala Met Asn Asp Val Gly Gly

100 105 110

Asp Ile Asn Lys Ile Asn Pro Glu Val Pro Val Asp Leu Val Ile Asp

115 120 125

His Ser Val Gln Val Asp Ser Tyr Ala Asn Pro Asp Ala Leu Gln Arg

130 135 140

Asn Met Lys Leu Glu Phe Glu Arg Asn Tyr Glu Arg Tyr Gln Phe Leu

145 150 155 160

Asn Trp Ala Thr Lys Ala Phe Asp Asn Tyr Asn Ala Val Pro Pro Ala

165 170 175

Thr Gly Ile Val His Gln Val Asn Leu Glu Tyr Leu Ala Asn Val Val

180 185 190

His Val Arg Asp Val Asp Gly Glu Gln Thr Ala Phe Pro Asp Thr Leu

195 200 205

Val Gly Thr Asp Ser His Thr Thr Met Ile Asn Gly Ile Gly Val Leu

210 215 220

Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Gly Met Leu Gly Gln

225 230 235 240

Pro Ser Tyr Phe Pro Ile Pro Glu Val Ile Gly Val Lys Leu Ser Asn

245 250 255

Glu Leu Pro Gln Gly Ser Thr Ala Thr Asp Leu Ala Leu Arg Val Thr

260 265 270

Glu Glu Leu Arg Lys Arg Gly Val Val Gly Lys Phe Val Glu Phe Phe

275 280 285

Gly Pr Gly Val Thr Asn Leu Pr Leu Ala Asp Arg Ala Thr Ile Ala

290 295 300

Asn Met Ala Pro Glu Tyr Gly Ala Thr Cys Gly Phe Phe Pro Val Asp

305 310 315 320

Glu Glu Ser Leu Lys Tyr Met Lys Leu Thr Gly Arg Lys Asp Asp His
325 330 335
Ile Ala Leu Val Lys Glu Tyr Leu Gln Gln Asn Asn Met Phe Phe Gln
340 345 350
Val Glu Asn Glu Asp Pro Glu Tyr Thr Glu Val Ile Asp Leu Asp Leu
355 360 365
Ser Thr Val Gln Ala Ser Leu Ser Gly Pro Lys Arg Pro Gln Asp Leu
370 375 380
Ile Phe Leu Ser Asp Met Lys Thr Glu Phe Glu Lys Ser Val Thr Ala
385 390 395 400
Pro Ala Gly Asn Gln Gly His Gly Leu Asp Glu Ser Glu Phe Asp Lys
405 410 415
Lys Ala Glu Ile Lys Phe Asn Asp Gly Arg Thr Ser Thr Met Lys Thr
420 425 430
Gly Asp Val Ala Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn
435 440 445
Pro Tyr Val Met Leu Gly Ala Gly Leu Val Ala Lys Lys Ala Ile Glu
450 455 460
Lys Gly Leu Lys Val Pro Asp Tyr Val Lys Thr Ser Leu Ala Pro Gly
465 470 475 480
Ser Lys Val Val Thr Gly Tyr Leu Arg Asp Ser Gly Leu Gln Glu Tyr
485 490 495
Leu Asp Asp Leu Gly Phe Asn Leu Val Gly Tyr Gly Cys Thr Thr Cys
500 505 510
Ile Gly Asn Ser Gly Pro Leu Leu Pro Glu Ile Glu Lys Ala Val Ala
515 520 525
Asp Glu Asp Leu Leu Val Thr Ser Val Leu Ser Gly Asn Arg Asn Phe
530 535 540
Glu Gly Arg Ile His Pro Leu Val Lys Ala Asn Tyr Leu Ala Ser Pr

545 550 555 560

Gln Leu Val Val Ala Tyr Ala Leu Ala Gly Thr Val Asp Ile Asp Leu

565 570 575

His Asn Glu Pro Ile Gly Lys Gly Lys Asp Gly Glu Asp Val Tyr Leu

580 585 590

Lys Asp Ile Trp Pro Ser Ile Lys Glu Val Ala Asp Thr Val Asp Ser

595 600 605

Val Val Thr Pro Glu Leu Phe Leu Glu Glu Tyr Ala Asn Val Tyr Glu

610 615 620

Asn Asn Glu Met Trp Asn Glu Ile Asp Val Thr Asp Ala Pro Leu Tyr

625 630 635 640

Asp Phe Asp Pro Asn Ser Thr Tyr Ile Gln Asn Pro Ser Phe Phe Gln

645 650 655

Gly Leu Ser Lys Glu Pro Gly Thr Ile Glu Pro Leu Lys Asp Leu Arg

660 665 670

Ile Met Gly Lys Phe Gly Asp Ser Val Thr Thr Asp His Ile Ser Pro

675 680 685

Ala Gly Ala Ile Gly Lys Asp Thr Pro Ala Gly Lys Tyr Leu Leu Asp

690 695 700

His Asp Val Pro Ile Arg Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly

705 710 715 720

Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg Ile Lys

725 730 735

Asn Gln Leu Ala Pro Gly Thr Glu Gly Gly Phe Thr Thr Tyr Trp Pro

740 745 750

Thr Glu Glu Ile Met Pro Ile Tyr Asp Ala Ala Met Arg Tyr Lys Glu

755 760 765

Asn Gly Thr Gly Leu Ala Val Leu Ala Gly Asn Asp Tyr Gly Met Gly

770 775 780

Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Val Lys
785 790 795 800
Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val
805 810 815
Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp
820 825 830
Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu
835 840 845
Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn
850 855 860
Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val
865 870 875 880
Glu Leu Asp Tyr Tyr Arg His Gly Gly Ile Leu Gln Met Val Leu Arg
885 890 895
Asn Lys Leu Ala Gln
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<210> 29

<211> 3006

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<213> Corynebacterium thermoaminogenes

<220>

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<222> (328)..(2514)

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ctggacagat cgcaggtggc attcatgggt tattggaggc agggagtggc catgaggggt 240
tgatatcgct tccctgaggg tccgcaggcg tgcctcaccc tgtattcttg atagttgaac 300
aaaagagccc acataacaag gagactc atg gct aag atc atc tgg acc cgc acc 354
Met Ala Lys Ile Ile Trp Thr Arg Thr
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gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag ccg gtc gtc gag 402
Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu
10 15 20 25
gct ttc gcc gcc acc gcg ggc atc gag gtg gag acc cgc gat atc tct 450
Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser
30 35 40
ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag 498
Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu
45 50 55
cag aag gtc tcc gac gcc ctc gcc gag ctc ggc gaa ctg gct aag acc 546
Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr
60 65 70
ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gta ccg 594
Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro
75 80 85
cag ctc aag gct gcc gta aag gaa ctg cag gaa cag ggc tac gac ctg 642
Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu
90 95 100 105
ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc 690
Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser
110 115 120
aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg 738
Asn Val Asn Pr Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pr

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          125                 130                 135
gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag   786
Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu
      140                 145                 150
tgg tcc gcc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac   834
Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp
  155                 160                 165
ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg   882
Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val
170                 175                 180                 185
gtg atc aag cat gtc gcc gcc gac ggc acc gag acc gtg ctc aag gac   930
Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp
                190                 195                 200
agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc   978
Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser
            205                 210                 215
gcc aag gca ctg gac gcc ttc ctg ctc gac cag gtc aaa cgc gcc aag   1026
Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys
        220                 225                 230
gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag   1074
Glu Glu Gly Ile Leu Phe Ser Ala His Met Lys Ala Thr Met Met Lys
    235                 240                 245
gtc tcc gac ccg atc atc ttc ggc cac atc gtc cgc gcc tac ttc gcc   1122
Val Ser Asp Pro Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala
250                 255                 260                 265
gat gtc tac gca cag tac ggt gag cag ctg ctc gcc gcc ggc ctc aac   1170
Asp Val Tyr Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn
                270                 275                 280
ggt gag aac ggt ctc gcc gcc atc tac gcc ggc ctg gac aag ctg gac   1218
```

```
Gly Glu Asn Gly Leu Ala Ala Ile Tyr Ala Gly Leu Asp Lys Leu Asp
            285                 290                 295
aac ggt gcc gag atc aag gca gcc ttc gac aag ggc ctg gaa gag ggc   1266
Asn Gly Ala Glu Ile Lys Ala Ala Phe Asp Lys Gly Leu Glu Glu Gly
        300                 305                 310
ccc gac ctg gcc atg gtg aac tcc gcc aag ggc atc acc aac ctg cat   1314
Pro Asp Leu Ala Met Val Asn Ser Ala Lys Gly Ile Thr Asn Leu His
    315                 320                 325
gtg ccc tcc gat gtc atc atc gac gcc tcc atg ccc gcc atg atc cgc   1362
Val Pro Ser Asp Val Ile Ile Asp Ala Ser Met Pro Ala Met Ile Arg
330                 335                 340                 345
acc tcc ggc aag atg tgg aac aag gac gac cag acc cag gat gcc ctg   1410
Thr Ser Gly Lys Met Trp Asn Lys Asp Asp Gln Thr Gln Asp Ala Leu
                350                 355                 360
gct gtc atc ccg gac tcc tcc tac gcc ggt gtc tac cag acc gtc atc   1458
Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile
            365                 370                 375
gag gac tgc cgc aag aat ggc gcc ttc gat ccg acc acc atg ggc acc   1506
Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr
        380                 385                 390
gtc ccc aac gtc ggt ctg atg gca cag aag gcc gag gag tac ggc tcc   1554
Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser
    395                 400                 405
cac gac aag acc ttc cgt atc gag gcc gac ggc aag gta cag gtc gtc   1602
His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Lys Val Gln Val Val
410                 415                 420                 425
gcc tcc aac ggt gat gtc ctc atc gag cac gac gtg gag aag ggc gac   1650
Ala Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Lys Gly Asp
                430                 435                 440
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atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac tgg gtc 1698
Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp Trp Val
445 450 455

aag ctg gct gtc aac cgc gca cgt ctc tcc ggc atg ccc gct gtg ttc 1746
Lys Leu Ala Val Asn Arg Ala Arg Leu Ser Gly Met Pro Ala Val Phe
460 465 470

tgg ctg gat ccc gcc cgc gca cac gac cgc aac ctg acc aca ctg gtg 1794
Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val
475 480 485

gag aag tac ctg gca gac cac gac acc gag ggc ctg gac atc cag atc 1842
Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile
490 495 500 505

ctc tcc ccc gtc gag gcc acc cag cac gcc atc gac cgc atc cgc cgc 1890
Leu Ser Pro Val Glu Ala Thr Gln His Ala Ile Asp Arg Ile Arg Arg
510 515 520

ggc gag gac acc atc tcc gtc acc ggt aac gtc ctg cgt gac tac aac 1938
Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn
525 530 535

acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag atg ctc 1986
Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu
540 545 550

tcc gtc gtg cca ctg atg gcc ggc ggt gga ctc ttc gag acc ggt gcc 2034
Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala
555 560 565

ggt ggc tcc gcc ccg aag cac gtc cag cag gtc atc gag gaa aac cac 2082
Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Ile Glu Glu Asn His
570 575 580 585

ctg cgc tgg gat tcc ctc ggt gag ttc ctg gcc ctg gcc gag tcc ttc 2130
L u Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe

```
                590                 595                 600
cgc cac gag ctc aac acc cgc aac aac acc aag gcc ggt gtc ctc gcc   2178
Arg His Glu Leu Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala
            605                 610                 615
gat gcc ctg gac cgt gcg acc gag aag ctc ctc aac gag gag aag tcc   2226
Asp Ala Leu Asp Arg Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser
        620                 625                 630
ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggt tcc cac ttc tgg   2274
Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp
    635                 640                 645
ctg gcc acc tac tgg gcc gat gaa ctg gcc aac cag acc gag gac gcc   2322
Leu Ala Thr Tyr Trp Ala Asp Glu Leu Ala Asn Gln Thr Glu Asp Ala
650                 655                 660                 665
gag ctg gct gag acc ttc gcc cct gtc gcc gag gcc ctg aac aac cag   2370
Glu Leu Ala Glu Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Asn Gln
                670                 675                 680
gct gcc gac atc gac gca gca ctc atc ggt gag cag ggc aag cct gtc   2418
Ala Ala Asp Ile Asp Ala Ala Leu Ile Gly Glu Gln Gly Lys Pro Val
            685                 690                 695
gac ctg ggt ggc tac tac gca ccc tcc gat gag aag acc tcc gcg atc   2466
Asp Leu Gly Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser Ala Ile
        700                 705                 710
atg cgc ccg gtg gcc gca ttc aac gag atc atc gac tcc ctg aag aag   2514
Met Arg Pro Val Ala Ala Phe Asn Glu Ile Ile Asp Ser Leu Lys Lys
    715                 720                 725
taacccctte tccggagccg acagccgacg gccacgctcc cccgcccacg ggggatcgtg 2574
gccgtcggcc gtttctggca ctggagtgaa cacttcggtg ataatggtga gatgaacagc 2634
ccccgtgtcc ccgccatcct gtccgccgtt tccgccgtgg gtctgatcgc tgcgctgggc 2694
acccccgttg ccgtcgcaga caccatcacc gcggacaccg accgggaaac ctgcgtggcc 2754
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agccagaatg acaactccag cgtgatcagg ttctgggatg acctggaggc cgatgtccgt 2814

gagcagcgcc tgaccgaact ggatgcacag gaccccggcc tcaagaacga catcgaggcc 2874

ttcatcgccg aggacccggt agccccctcc gcagccgatc tccagagacg gctggatgca 2934

aatgacgccg gtgagggcct ggccatgctg ctacctgaat cccgcaccga ccccgaggtg 2994

gtggacctgc ag 3006

[0096]

<210> 30

<211> 729

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 30

Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
1 5 10 15

Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
20 25 30

Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
35 40 45

Gln Phe Ala Asp Gln Leu Pro Glu Glu Gln Lys Val Ser Asp Ala Leu
50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Val Lys
85 90 95

Glu Leu Gln Glu Gln Gly Tyr Asp Leu Pro Glu Tyr Glu Asp Ala Lys
100 105 110

Asp Arg Tyr Ala Ala Val Ile Gly Ser Asn Val Asn Pr Val Leu Arg
115 120 125

Glu Gly Asn Ser Asp Arg Arg Ala Pro Val Ala Val Lys Asn Phe Val

130 135 140

Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala Asp Ser Lys Thr

145 150 155 160

Asn Val Ala Thr Met Gly Ala Asp Asp Phe Arg Ser Asn Glu Lys Ser

165 170 175

Val Ile Met Asp Glu Ala Asp Thr Val Val Ile Lys His Val Ala Ala

180 185 190

Asp Gly Thr Glu Thr Val Leu Lys Asp Ser Leu Pro Leu Leu Lys Gly

195 200 205

Glu Val Ile Asp Gly Thr Phe Ile Ser Ala Lys Ala Leu Asp Ala Phe

210 215 220

Leu Leu Asp Gln Val Lys Arg Ala Lys Glu Glu Gly Ile Leu Phe Ser

225 230 235 240

Ala His Met Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe

245 250 255

Gly His Ile Val Arg Ala Tyr Phe Ala Asp Val Tyr Ala Gln Tyr Gly

260 265 270

Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala

275 280 285

Ile Tyr Ala Gly Leu Asp Lys Leu Asp Asn Gly Ala Glu Ile Lys Ala

290 295 300

Ala Phe Asp Lys Gly Leu Glu Glu Gly Pro Asp Leu Ala Met Val Asn

305 310 315 320

Ser Ala Lys Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Ile

325 330 335

Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly Lys Met Trp Asn

340 345 350

Lys Asp Asp Gln Thr Gln Asp Ala Leu Ala Val Ile Pro Asp Ser Ser

355 360 365

Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly
370 375 380
Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met
385 390 395 400
Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile
405 410 415
Glu Ala Asp Gly Lys Val Gln Val Val Ala Ser Asn Gly Asp Val Leu
420 425 430
Ile Glu His Asp Val Glu Gly Asp Ile Trp Arg Ala Cys Gln Thr
435 440 445
Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Asn Arg Ala
450 455 460
Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Ala Arg Ala
465 470 475 480
His Asp Arg Asn Leu Thr Thr Leu Val Glu Lys Tyr Leu Ala Asp His
485 490 495
Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro Val Glu Ala Thr
500 505 510
Gln His Ala Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val
515 520 525
Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu Phe Pro Ile Leu
530 535 540
Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val Pro Leu Met Ala
545 550 555 560
Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His
565 570 575
Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly
580 585 590
Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg

595 600 605

Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr

610 615 620

Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu

625 630 635 640

Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp

645 650 655

Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala

660 665 670

Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala

675 680 685

Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala

690 695 700

Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe

705 710 715 720

Asn Glu Ile Ile Asp Ser Leu Lys Lys

725

【００９７】

<210> 31

<211> 2322

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (806)..(2212)

<400> 31

ggtaccccca cgtaccctag gccatcacag caatttttac atcggatatt ttaggtgtgc 60

tcataacgtc cttatgaatt tcgcagttat tagttattta aatagagaat caaactccga 120

cctagcctct gccgatgcta aaagtcagct gacccccttgg ggcgcttcat ttgaaactgc 180

gaccaagctc atgaatgcgc gaaagcattt ccattataag ggtaagctgt aagaatagtg 240

ggagaaaatg ttcagtcgtg ttctaactca cttgagaaat tccatttttc tgggcttctc 300

tcaaatagat taagtggccc gtatgctgga tttctagaat atttagaagc gcgccaactc 360

atgattatgt attgtataag cctcaaagac cgaatagatt actaacattt aagtggacca 420

gagcgttaga agctttgtag agtgctcatt ccttgctgac ggcaagggtt tcctaccatg 480

agatagatcg gcagatagtt ggtttgtaaa aatttttaag gacggtccgc aatgtcaatt 540

cttgaacaga tcatcttctt catcaacacc atcttgggtt atggtctgca cgctggttct 600

tccgcttcca gcaacctttc tcacacgatc ggcctgttct aggcctaatt ggtaataagg 660

ctgtgtaaca gtcgcccgcg tgattgtgtc tttttaggcg cccgcgcggg cgattttcgg 720

ttttcatctt ttttaaattg agtttggaag atcaagtgcc cccggatgca cgacaatgct 780

atgccgaaca cgtattgttg aaatc gtg act gaa cat tat gac gta gta gta 832

Val Thr Glu His Tyr Asp Val Val Val

1 5

ctc gga gct ggc ccc ggt ggc tat gtc tcc gcc atc cgc gcc gcg cag 880

Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile Arg Ala Ala Gln

10 15 20 25

ctc ggt aag aaa gtt gcg gtt atc gag aag cag tac tgg gga ggt gtc 928

Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr Trp Gly Gly Val

30 35 40

tgc ctg aat gtg ggt tgt atc cca tct aag gcg ttg atc aag aac gct 976

Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Ile Lys Asn Ala

45 50 55

gag atc gcc cac atc ttc aac cat gag aag aag acc ttc ggc atc aac 1024

Glu Ile Ala His Ile Phe Asn His Glu Lys Lys Thr Phe Gly Ile Asn

60 65 70

ggc gag gtc acc ttc aac tac gag gat gcc cac aag cgt tcc cgt ggt 1072

Gly Glu Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly

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    75                  80                  85
gtc tcc gac aag atc gtc ggc ggt gtt cac tac ttg atg aag aag aac   1120
Val Ser Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn
 90                  95                 100                 105
aag atc acc gag atc gac ggt ttc ggc acc ttc aag gat gcc aag acc   1168
Lys Ile Thr Glu Ile Asp Gly Phe Gly Thr Phe Lys Asp Ala Lys Thr
                110                 115                 120
atc gag gtg acc gat ggt aag gat gcc ggc aag acc gtc acc ttc gat   1216
Ile Glu Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Val Thr Phe Asp
            125                 130                 135
gac tgc atc atc gcc acc ggt tcc gtg gtc aac tcc ctc cgt ggt gtt   1264
Asp Cys Ile Ile Ala Thr Gly Ser Val Val Asn Ser Leu Arg Gly Val
        140                 145                 150
gag ttc tcc gag aac gtg gtc tcc tac gag gag cag atc ctc aac ccg   1312
Glu Phe Ser Glu Asn Val Val Ser Tyr Glu Glu Gln Ile Leu Asn Pro
    155                 160                 165
gtg gcg cct aag aag atg gtc atc gtc ggt ggc ggc gcc atc ggt atg   1360
Val Ala Pro Lys Lys Met Val Ile Val Gly Gly Gly Ala Ile Gly Met
170                 175                 180                 185
gaa ttc gcc tac gtt ctg ggc aac tac ggt gtg gac gta acc ctc atc   1408
Glu Phe Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Leu Ile
                190                 195                 200
gag ttc atg gac cgc gtt ctg ccg aac gag gat cca gag gtg tcc aag   1456
Glu Phe Met Asp Arg Val Leu Pro Asn Glu Asp Pro Glu Val Ser Lys
            205                 210                 215
gtt atc gcc aag gcc tac aag aag atg ggc atc aag ctc ctc ccg ggc   1504
Val Ile Ala Lys Ala Tyr Lys Lys Met Gly Ile Lys Leu Leu Pro Gly
        220                 225                 230
cac gca acc acc gcg gtg cgc gac aat ggc gat tcc gtt gag gtc gat   1552
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His Ala Thr Thr Ala Val Arg Asp Asn Gly Asp Ser Val Glu Val Asp
    235                 240                 245
tac cag aag aag ggc tcg gac aag acc gag acc atc acc gtc gac cgt   1600
Tyr Gln Lys Lys Gly Ser Asp Lys Thr Glu Thr Ile Thr Val Asp Arg
250                 255                 260                 265
gtt ctt atc tcc gtc ggc ttc cgc cca cgc gtc gag ggc ttc ggc ctg   1648
Val Leu Ile Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu
                270                 275                 280
gag aac acc ggc gtc aag ctc acc gaa cgc ggt gcc atc gac att gat   1696
Glu Asn Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Asp Ile Asp
            285                 290                 295
gag cat atg cgc acc aac gtc gac ggc atc tac gcc atc ggt gac gtc   1744
Glu His Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val
        300                 305                 310
acc gcc aag ctg cag ctg gca cac gtc gcc gag gca cag ggc att gtc   1792
Thr Ala Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val
    315                 320                 325
gcc gcc gag aca ctc gcc ggc gca gaa acc cag acc ctg ggc gac tac   1840
Ala Ala Glu Thr Leu Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr
330                 335                 340                 345
atg atg atg ccg cgt gcc acc ttc tgc aac cca cag gtt gcc tcc ttc   1888
Met Met Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ala Ser Phe
                350                 355                 360
ggt tac acc gag gag cag gcc aag gag aag tgg ccg gat cga gag atc   1936
Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile
            365                 370                 375
aag gtg tcc tcc ttc ccg ttc tcc gcg aac ggc aag gcc gtc ggc ctg   1984
Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu
        380                 385                 390
```

gct gag acc gat ggt ttc gcc aag atc gtc gcc gac gct gag ttc ggt 2032
Ala Glu Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly
395 400 405

gaa ctg ctg ggt ggc cac att gtc ggt gcc aac gcc tcc gag ctg ctc 2080
Glu Leu Leu Gly Gly His Ile Val Gly Ala Asn Ala Ser Glu Leu Leu
410 415 420 425

aac gag ctg gtg ctg gcc cag aac tgg gat ctc acc acc gag gag atc 2128
Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile
430 435 440

agc cgc agc gtc cac atc cac ccg acc ctg tcg gag gct gtc aag gaa 2176
Ser Arg Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu
445 450 455

gct gcc cac ggc gtc aac ggc cac atg atc aac ttc taaatcccgt 2222
Ala Ala His Gly Val Asn Gly His Met Ile Asn Phe
460 465

cagacaaatg caaatcccct caccgatggc atatcggtga ggggatttтc tcatgcacgt 2282

aaaatcataa tccatggcaa ggaaagtcga caacagcgcc 2322

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<210> 32

<211> 469

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 32

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1 5 10 15

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
20 25 30

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile

35 40 45

Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Asn

50 55 60

His Glu Lys Lys Thr Phe Gly Ile Asn Gly Glu Val Thr Phe Asn Tyr

65 70 75 80

Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly

85 90 95

Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly

100 105 110

Phe Gly Thr Phe Lys Asp Ala Lys Thr Ile Glu Val Thr Asp Gly Lys

115 120 125

Asp Ala Gly Lys Thr Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly

130 135 140

Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val

145 150 155 160

Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val

165 170 175

Ile Val Gly Gly Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly

180 185 190

Asn Tyr Gly Val Asp Val Thr Leu Ile Glu Phe Met Asp Arg Val Leu

195 200 205

Pro Asn Glu Asp Pro Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys

210 215 220

Lys Met Gly Ile Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg

225 230 235 240

Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp

245 250 255

Lys Thr Glu Thr Ile Thr Val Asp Arg Val Leu Il Ser Val Gly Phe

260 265 270

Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
275 280 285
Thr Glu Arg Gly Ala Ile Asp Ile Asp Glu His Met Arg Thr Asn Val
290 295 300
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305 310 315 320
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Leu Ala Gly
325 330 335
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
340 345 350
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Glu Gln Ala
355 360 365
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ser Ser Phe Pro Phe
370 375 380
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
385 390 395 400
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Gly His Ile
405 410 415
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
420 425 430
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
435 440 445
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Val Asn Gly
450 455 460
His Met Ile Asn Phe
465

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<210> 33

<211> 4096

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222>-(250)..(3951)

<400> 33

ccggatcatc gtggttgacg ggggacgtat catcgaggat ggttcccacg atgaacttct 60

gggagcgaat ggaacctacg caacaatgtg gcatttagta gggtgacagg atattttagg 120

aaagacttgt taccaaaagg tgctaatact ggggtgctag gtccccgcga ccggaaccag 180

cgttacagtg gataaaataa agcccattta gaaccctcaa caagcaagga aaagaggcga 240

gtacctgcc gtg agc agc gct agt act ttc ggc cag aac gcg tgg ctg gtg 291

Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val

1 5 10

gat gag atg ttc cag cag ttc aag aag gac ccc cag tcc gtg gac aag 339

Asp Glu Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys

15 20 25 30

gaa tgg aga gag ctc ttc gag tct cag ggg ggt ccc cag gct gaa aag 387

Glu Trp Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys

35 40 45

gct acc ccc gcc acc ccc gaa gcc aag aag gca gct tcg tcg cag tcc 435

Ala Thr Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser

50 55 60

tca act tcc gga cag tcc acc gcc aag gct gcc cct gcc gcc aag acc 483

Ser Thr Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr

65 70 75

gca ccg gcc tct gcg cca gcc aag gct gcc cct gtt aag caa aac cag 531

Ala Pr Ala Ser Ala Pr Ala Lys Ala Ala Pr Val Lys Gln Asn Gln

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     80                  85                  90
gcg tcc aag cct gcc aag aag gcc aag gag tcc ccc ctg tcc aag cca   579
Ala Ser Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro
 95                 100                 105                 110
gct gcc atg cct gag ccg gga acc acc cca ctc agg ggc atc ttc aag   627
Ala Ala Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys
                115                 120                 125
tcc atc gcc aag aac atg gac ctc tcc ctc gag gtg ccc acc gcc acc   675
Ser Ile Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr
            130                 135                 140
tcc gtc cgc gac atg ccc gcg cgc ctc atg ttc gag aac cgc gcc atg   723
Ser Val Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met
        145                 150                 155
gtc aac gac cag ctc aag cgc acc cgt ggc ggc aag atc tcc ttc acc   771
Val Asn Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr
    160                 165                 170
cac atc atc ggc tac gcc atg gtg aag gct gtc atg gca cac ccg gac   819
His Ile Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp
175                 180                 185                 190
atg aac aac tcc tat gac atc gtc gac ggc aag ccg tcc ctg gtc gtc   867
Met Asn Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val
                195                 200                 205
ccg gag cac atc aac ctc ggc ctg gcc atc gac ctc ccc cag aag gac   915
Pro Glu His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp
            210                 215                 220
ggc tcc cgt gcc ctc gtg gtc gcc gcc atc aag gaa acc gag aag atg   963
Gly Ser Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met
        225                 230                 235
acc ttc tcc cag ttc ctg gag gcc tat gag gac gtt gtg gca cgc tcc   1011
```

```
Thr Phe Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser
    240                 245                 250
cgc gtc ggc aag ctc acc atg gat gac tac cag ggt gtc acc atc tcc   1059
Arg Val Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser
255                 260                 265                 270
ttg acc aac ccg ggt ggc atc ggt acc cgc cac tcc atc ccg cgt ctg   1107
Leu Thr Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu
                275                 280                 285
acc aag ggc cag ggc acc atc atc ggt gtc ggt tcc atg gac tac ccg   1155
Thr Lys Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro
            290                 295                 300
gcc gag ttc cag ggt gcc tcc gag gac cgt ctc gcc gag ctc ggt gtg   1203
Ala Glu Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val
        305                 310                 315
ggc aag ctc gtc acc atc acc tcc acc tac gat cac cgc gtc atc cag   1251
Gly Lys Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln
    320                 325                 330
ggc gcg gaa tcc ggt gag ttc ctg cgc acc atg tcc cag ctg ctc gtg   1299
Gly Ala Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val
335                 340                 345                 350
gac gat gcg ttc tgg gat cac atc ttc gag gag atg aac gtt ccc tac   1347
Asp Asp Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr
                355                 360                 365
acc ccg atg cgc tgg gca cag gac ctg ccc aac acc ggt gtg gac aag   1395
Thr Pro Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys
            370                 375                 380
aac acc cgt gtc atg cag ctc atc gag gcc tac cgc tcc cgc ggt cac   1443
Asn Thr Arg Val Met Gln Leu Ile Glu Ala Tyr Arg S r Arg Gly His
        385                 390                 395
```

```
ctc atc gcc gac acc aac cca ctg ccc tgg gtc cag ccc ggc atg ccc   1491
Leu Ile Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro
    400                 405                 410
gtc ccg gat cac cgt gac ctc gac atc gag acc cac ggc ctg acc ctg   1539
Val Pro Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu
415                 420                 425                 430
tgg gat ctg gac cgt acc ttc cac gtc ggt ggt ttc ggt ggc aag gag   1587
Trp Asp Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu
                435                 440                 445
acc atg acc ctg cgc gag gtg ctc agc cgc ctc cgc gcc gcc tac acc   1635
Thr Met Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr
            450                 455                 460
ctc aag gtc ggc tcc gag tac acc cac atc ctc gac cgc gat gag cgc   1683
Leu Lys Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg
        465                 470                 475
acc tgg ctg cag gac cgc ctc gag gcc ggt atg ccc aag ccc acc gcc   1731
Thr Trp Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala
    480                 485                 490
gcc gag cag aag tac atc ctg cag aag ctc aac gcc gcc gag gca ttc   1779
Ala Glu Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe
495                 500                 505                 510
gag aac ttc ctg cag acc aag tac gtc ggc cag aag cgt ttc tcc ctc   1827
Glu Asn Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu
                515                 520                 525
gag ggt gcc gag tca ctg atc ccg ctg atg gac tcc gcc atc gac acc   1875
Glu Gly Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr
            530                 535                 540
gcc gca ggc cag ggc ctt gac gag gtc gtc atc ggc atg ccc cac cgt   1923
Ala Ala Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pr  His Arg
```

```
        545                 550                 555
ggt cgc ctc aac gtg ctg ttc aac atc gtc ggc aag cca ctg gcc tcg   1971
Gly Arg Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser
    560                 565                 570
atc ttc aac gag ttc gag ggc cag atg gag cag ggc cag atc ggt ggc   2019
-Ile-Phe-Asn-Glu Phe-Glu Gly-Gln-Met-Glu-Gln-Gly-Gln-Ile Gly Gly
575                 580                 585                 590
tcc ggt gac gtg aag tac cac ctc ggt tcc gag ggc acc cac ctg cag   2067
Ser Gly Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln
                595                 600                 605
atg ttc ggc gac ggc gag atc aag gtc tcc ctc acc gcc aac ccc tcc   2115
Met Phe Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser
            610                 615                 620
cac ctc gag gcc gtc aac ccg gtc gtg gag ggc atc gtc cgc gcc aag   2163
His Leu Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys
        625                 630                 635
cag gac atc ctg gac aag ggc ccg gac ggc tac acc gtc gtc ccg ctg   2211
Gln Asp Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu
    640                 645                 650
ctg ctc cac ggt gac gcc gcc ttc gcc ggc ctg ggc atc gtg ccc gag   2259
Leu Leu His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu
655                 660                 665                 670
acc atc aac ctc gca gcc ctg cgt ggt tac gat gtc ggt ggc acc atc   2307
Thr Ile Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile
                675                 680                 685
cac atc gtg gtc aac aac cag atc ggc ttc acc acc acc ccg gac tcc   2355
His Ile Val Val Asn Asn Gln Ile Gly Phe Thr Thr Thr Pro Asp Ser
            690                 695                 700
agc cgt tcc atg cac tac gcc acc gac tgc gcc aag gcc ttc ggt tgc   2403
```

```
Ser Arg Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys
        705                 710                 715
ccg gtg ttc cac gtc aac ggt gac gac ccc gag gct gtg gtc tgg gtc   2451
Pro Val Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val
    720                 725                 730
ggc cag ctg gcc acc gag tac cgt cgc cgc ttc ggc aag gat gtc ttc   2499
Gly Gln Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe
735                 740                 745                 750
atc gac ctc atc tgc tac cgc ctg cgc ggc cac aac gag gct gat gac   2547
Ile Asp Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp
                755                 760                 765
cca tcc atg acc cag ccg aag atg tac gag ctg atc acc ggc cgc gac   2595
Pro Ser Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp
            770                 775                 780
tcc gtg cgt gcc acc tac acc gag gac ctc ctc ggc cgt ggt gac ctc   2643
Ser Val Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu
        785                 790                 795
tcc ccc gag gac gcc gag gcc gtt gtc cgc gac ttc cac gac cag atg   2691
Ser Pro Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met
    800                 805                 810
gaa tcc gtg ttc aac gag gtc aag gaa gcc ggc aag aag cag cct gat   2739
Glu Ser Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp
815                 820                 825                 830
gag cag acc ggc atc acc ggt tcc cag gaa ctg acc cgt ggc ctg gac   2787
Glu Gln Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp
                835                 840                 845
acc aac atc acc cgc gag gaa ctg gtc gaa ctc ggc cag gcc ttc gtc   2835
Thr Asn Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val
            850                 855                 860
```

```
aac acc cca gag ggc ttc acc tac cac cca cgt gtg gca ccg gtg gcc   2883
Asn Thr Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala
        865                 870                 875
aag aag cgt gcc gag tcc gtc acc gag ggt ggc atc gac tgg gca tgg   2931
Lys Lys Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp
    880                 885                 890
ggc gag ctc atc gcc ttc ggc tcc ctg gcc acc tcc ggc agg ctg gtc   2979
Gly Glu Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val
895                 900                 905                 910
cgc ctc gcc ggt gag gat tcc cgc cgt ggt acc ttc acc cag cgt cac   3027
Arg Leu Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His
                915                 920                 925
gcc gtg gcc atc gac ccg aac acc gcc gag gag ttc aac ccg ctc cac   3075
Ala Val Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His
            930                 935                 940
gag ctg gca cag gcc aag ggc ggc ggc aag ttc ctc gtc tac aac tcc   3123
Glu Leu Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser
        945                 950                 955
gcg ctg acc gag tac gcg ggt atg ggc ttc gaa tac ggc tac tcc gtg   3171
Ala Leu Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val
    960                 965                 970
ggc aac ccg gac gcc gtg gtg tcc tgg gag gca cag ttc ggt gac ttc   3219
Gly Asn Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe
975                 980                 985                 990
gcc aac ggt gca cag acc atc atc gat gag tac atc tcc tcc ggt gag   3267
Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu
                995                1000                1005
gcc aag tgg ggc cag acc tcc tcg gtc atc ctg ctg ctg ccc cac ggt   3315
Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly
```

```
          1010                1015                1020
tac gag ggc cag ggt ccg gac cac tcc tcc gca cgc atc gag cgt ttc   3363
Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe
       1025                1030                1035
ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc   3411
Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr
   1040                1045                1050
ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg   3459
Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met
1055                1060                1065                1070
aag cgc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag   3507
Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys
                1075                1080                1085
gcc gcc acc tcc gct ccg gag gag ttc acc gag gtc acc cgc ttc aag   3555
Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys
          1090                1095                1100
tcc gtg atc gac gat ccg aac gtg gcg gat gcc tcc aag gtg aag aag   3603
Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys
       1105                1110                1115
atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag   3651
Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys
   1120                1125                1130
gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg   3699
Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu
1135                1140                1145                1150
cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac ggc tac ccc   3747
His Pr  Ile Pr  Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pr
                1155                1160                1165
aac gcc gag gag atc ctg ttc gtt cag gac gag ccg gca aac cag ggt   3795
```

Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly
1170 1175 1180

gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctc atc gag ggc atg 3843
Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met
1185 1190 1195

ctc ccg atg cgt cgc atc tcg cgc cgt tcc cag tcc tcg act gcg acc 3891
Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr
1200 1205 1210

ggt atc gcg aag gtg cac acc atc gag cag cag aag ctg ctg gat gat 3939
Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp
1215 1220 1225 1230

gcg ttc aac gca taaacgttaa tacagcggtt gataccttga accccgccgc 3991
Ala Phe Asn Ala

acccttttaga tgcgggcggg gttttgcttt gcctgcatag gcgataatat tcatatacac 4051

ccatcacgtt taagttctgc atttggatcg tgcgagcatc ccggt 4096

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<210> 34

<211> 1234

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 34

Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val Asp Glu
1 5 10 15

Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys Glu Trp
20 25 30

Arg Glu Leu Phe Glu Ser Gln Gly Gly Pr Gln Ala Glu Lys Ala Thr
35 40 45

Pr Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser Ser Thr

```
     50                  55                  60
Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr Ala Pro
 65                  70                  75                  80
Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln Ala Ser
                 85                  90                  95
Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro Ala Ala
            100                 105                 110
Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys Ser Ile
        115                 120                 125
Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr Ser Val
    130                 135                 140
Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met Val Asn
145                 150                 155                 160
Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr His Ile
                165                 170                 175
Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp Met Asn
            180                 185                 190
Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val Pro Glu
        195                 200                 205
His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp Gly Ser
    210                 215                 220
Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met Thr Phe
225                 230                 235                 240
Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser Arg Val
                245                 250                 255
Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser Leu Thr
            260                 265                 270
Asn Pr  Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu Thr Lys
        275                 280                 285
```

Gly Gln Gly Thr Ile Ile Gly Val Gly S r Met Asp Tyr Pro Ala Glu
290 295 300
Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val Gly Lys
305 310 315 320
Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln Gly Ala
325 330 335
Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val Asp Asp
340 345 350
Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr Thr Pro
355 360 365
Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys Asn Thr
370 375 380
Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His Leu Ile
385 390 395 400
Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro Val Pro
405 410 415
Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu Trp Asp
420 425 430
Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu Thr Met
435 440 445
Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr Leu Lys
450 455 460
Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg Thr Trp
465 470 475 480
Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala Ala Glu
485 490 495
Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe Glu Asn
500 505 510
Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu Glu Gly

515 520 525

Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr Ala Ala

530 535 540

Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg Gly Arg

545 550 555 560

Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser Ile Phe

565 570 575

Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly Ser Gly

580 585 590

Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln Met Phe

595 600 605

Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser His Leu

610 615 620

Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys Gln Asp

625 630 635 640

Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu Leu Leu

645 650 655

His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu Thr Ile

660 665 670

Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile His Ile

675 680 685

Val Val Asn Asn Gln Ile Gly Phe Thr Thr Thr Pro Asp Ser Ser Arg

690 695 700

Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys Pro Val

705 710 715 720

Phe His Val Asn Gly Asp Asp Pr Glu Ala Val Val Trp Val Gly Gln

725 730 735

Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe Ile Asp

740 745 750

Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp Pro Ser
755 760 765
Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp Ser Val
770 775 780
Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu Ser Pro
785 790 795 800
Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met Glu Ser
805 810 815
Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp Glu Gln
820 825 830
Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp Thr Asn
835 840 845
Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val Asn Thr
850 855 860
Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala Lys Lys
865 870 875 880
Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp Gly Glu
885 890 895
Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val Arg Leu
900 905 910
Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His Ala Val
915 920 925
Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His Glu Leu
930 935 940
Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu
945 950 955 960
Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn
965 970 975
Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn

980 985 990

Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu Ala Lys

995 1000 1005

Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly Tyr Glu

1010 1015 1020

Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln

025 1030 1035 1040

Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr Pro Ala

1045 1050 1055

Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met Lys Arg

1060 1065 1070

Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys Ala Ala

1075 1080 1085

Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys Ser Val

1090 1095 1100

Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys Ile Met

105 1110 1115 1120

Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys

1125 1130 1135

Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu His Pro

1140 1145 1150

Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala

1155 1160 1165

Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp

1170 1175 1180

Pro Phe Tyr Gln Glu His Leu Pr Asn Leu Ile Glu Gly Met Leu Pr

185 1190 1195 1200

Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile

1205 1210 1215

Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe
1220 1225 1230

Asn Ala

【０１０１】

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for aceA

<400> 35

cctctaccca gcgaactccg 20

【０１０２】

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for aceA

<400> 36

ctgccttgaa ctcacggttc 20

【０１０３】

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for accBC

<400> 37

catccacccc ggctacggct 20

【０１０４】

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for accBC

<400> 38

cggtgactgg gtgttccacc 20

【０１０５】

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer f r dtsR1

<400> 39

acggcccagc cctgaccgac 20

【０１０６】

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dtsR1

<400> 40

agcagcgccc atgacggcga 20

【０１０７】

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dtsR2

<400> 41

acggcccagc cctgaccgac 20

【０１０８】

<210> 42

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dtsR2

<400> 42

agcagcgccc atgacggcga 20

【０１０９】

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pfk

<400> 43

cgtcatccga ggaatcgtcc 20

【０１１０】

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pfk

<400> 44

cgtggcggcc catgacctcc 21

【０１１１】

<210> 45

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for scrB

<220>

<221> UNSURE

<222> (3)

<223> n=a or g or c or t

<400> 45

ggncghytba aygaycc 17

【０１１２】

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for scrB

<220>

<221> UNSURE

<222> (18)

<223> n=a or g or c or t

<400> 46

ggrcaytccc acatrtancc 20

【０１１３】

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 47

ccatccggat ccggcaagtc 20

【０１１４】

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 48

aatcccatct cgtgggtaac 20

【０１１５】

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 49

actgtgtcca tgggtcttgg ccc 23

【０１１６】

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 50

cgctggaatccgaacatcga 20

【０１１７】

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 51

ggcgcaacct acgacgttgc aatgcg 26

【０１１８】

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 52

tggccgcctg ggatctcgtg 20

【０１１９】

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for ppc

<400> 53

ggttcctgga ttggtggaga 20

【０１２０】

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description f Artificial Sequence: primer f r ppc

<400> 54

ccgccatcct tgttggaatc 20

【０１２１】

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for acn

<220>

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<222> (3,6,9)

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gtnggnacng aytcscatac 20

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<210> 56

<211> 20

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for acn

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<222> (3,9,18)

<223> n=inosine

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gcnggagana tgtgrtcngt 20

【０１２３】

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for icd

<400> 57

gacatttcac tcgctggacg 20

【０１２４】

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for icd

<400> 58

ccgtactctt cagccttctg 20

【０１２５】

<210> 59

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for lpd

<400> 59

atcatcgcaa ccggttc 17

【０１２６】

<210> 60

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for lpd

<400> 60

cgtcaccgat ggcgtaaat 19

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<210> 61

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for dhA

<400> 61

acaccgtggt cgcctcaacg 20

【０１２８】

<210> 62

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for odhA

<400> 62

tgctaacccg tcccacctgg 20

【０１２９】

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for screening PCR of lpd

<400> 63

tacgaggagc agatcctcaa 20

【０１３０】

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for screening PCR of lpd

<400> 64

ttgacgccgg tgttctccag 20

【０１３１】

<210> 65

<211> 20

<212> DNA

<213> Artificial Sequence

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<400> 65

ggtgaagcta agtagttagc 20

【０１３２】

<210> 66

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Descripti n of Artificial Sequence: primer f r LA cloning of acn

<400> 66

agctactaaa cctgcacc 18

【０１３３】

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for LA cloning of icd

<400> 67

ccgtactctt cagccttctg 67

【０１３４】

<210> 68

<211> 18

<212> DNA

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<223> Description of Artificial Sequence: primer for LA cloning of icd

<400> 68

tcgtccttgt tccacatc 18

【０１３５】

<210> 69

<211> 17

<212> DNA

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<400> 69

atcatcgcaa ccggttc 17

【０１３６】

<210> 70

<211> 20

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<400> 70

tacgaggagc agatcctcaa 20

【０１３７】

<210> 71

<211> 20

<212> DNA

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LA cloning of acn

<400> 71

gctaactact tagcttcacc 20

【０１３８】

<210> 72

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 72

gaaccaggaa ctattgaacc 20

【０１３９】

<210> 73

<211> 18

<212> DNA

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<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 73

tccgatgtca tcatcgac 18

【０１４０】

<210> 74

<211> 18

<212> DNA

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<400> 74

atgtggaaca aggacgac 18

【０１４１】

<210> 75

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for LA cloning of odhA

<400> 75

gtacatattg tcgttagaac gcgtaatacg actca 35

【０１４２】

<210> 76

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for LA cloning of odhA

<400> 76

cgttagaacg cgtaatacga ctcactatag ggaga 35

【書類名】　　要約書

【要約】

【課題】コリネバクテリウム・サーモアミノゲネス由来のＬ－アミノ酸生合成系酵素、好ましくはコリネバクテリウム・グルタミカムよりも高い温度で機能する酵素をコードする遺伝子を提供する。

【解決手段】　目的とする遺伝子に対応する種々の微生物の既知の遺伝子配列の間でアミノ酸レベルで保存されている領域に基づいて設計した複数組のプライマーとして、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡを鋳型としてＰＣＲを行い、増幅断片が得られたプライマーをスクリーニング用プライマーに用いて、コリネバクテリウム・サーモアミノゲネスの染色体ＤＮＡのプラスミドライブラリーから、目的とするＤＮＡ断片を含むクローンを選択する。

【選択図】　なし

出証特２０００－３０９３６１３

出 願 人 履 歴 情 報

識別番号　〔０００００００６６〕

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